

(TM)

Release 3.1a John F. Collins, Biocomputing Research Unit.
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MPerch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Jan 18 14:34:21 2000; MasPar time 4137.75 Seconds

Tabular output not generated. 1382.878 Million cell updates/sec

Title: >US-09-246-129-1
Description: (1-2442) from US09246129A.seq
Perfect Score: 2436
N.A. Sequence: 1 cccaatcaagaagaattcca.....tccaaaaa.....2442
Comp: 99gttagctctcttaagt.....agtttttttttttttt

Scoring table: TABLE default
Gap 6

Mmatch STD : Dbase 0; Query 0

Searched: 2883791 seqs, 1171580779 bases x 2

Post-processing: Minimum Match 08
Listing first 45 summaries

Database:

emb1-est58
1:em-est10 2:em-est11 3:em-est17 4:em-est18 5:em-est2
6:em-est9 7:em-gss1
Database:
8:gb-est1 9:gb-est10 10:gb-est11 11:gb-est12 12:gb-est13
13:gb-est14 14:gb-est15 15:gb-est16 16:gb-est17
17:gb-est18 18:gb-est19 19:gb-est20 20:gb-est21
21:gb-est22 22:gb-est23 23:gb-est24 24:gb-est25
25:gb-est26 26:gb-est27 27:gb-est28 28:gb-est29
29:gb-est30 30:gb-est31 31:gb-est32 32:gb-est33 33:gb-est34
34:gb-est35 35:gb-est36 36:gb-est37 37:gb-est38 38:gb-est39
39:gb-est40 40:gb-est41 41:gb-est42 42:gb-est43

Statistics: Mean 12.370; Variance 3.440; scale 3.596

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
c 1	221	9.1	340 40	AQ230483	HS-2041.B1.B07.MR.CIT	1.49e-266
c 2	222	9.1	389 42	AQ429198	CITB1-ET-2581D3.TF.CIT	4.98e-268
c 3	216	8.9	556 41	AQ372425	RPC111-143N11.TV.RPC11	3.56e-259
c 4	217	8.9	938 42	AF101690	Homo sapiens chromosome	1.19e-260
c 5	214	8.8	325 14	AA557945	n117b07.s1.NCI.CGAP.HS	3.16e-256
c 6	214	8.8	352 29	AI572680	tr78a09.x1.NCI.CGAP.Pa	3.16e-257
c 7	215	8.8	421 15	AA569220	nm30h04.s1.NCI.CGAP.Li	1.06e-257
c 8	214	8.8	432 39	AA093841	HS-3023.B2.G10.T7.CIT	3.16e-256
c 9	215	8.8	454 28	AI567676	tr64d05.x1.NCI.CGAP.Pa	1.06e-257
c 10	214	8.8	516 41	AQ347616	RPC111-126024.TV.RPC11	3.16e-256

c 11	214	8.8	623 42	AQ377046	RPC111-151M17.TV.RPC11	3.16e-256
c 12	214	8.8	730 42	AQ383774	RPC111-139B6.TV.RPC11	3.16e-256
c 13	214	8.8	762 41	AQ311398	CITB1-ET-2527N10.TF.CI	3.16e-256
c 14	211	8.7	347 39	AQ098015	HS-3041.A1.H02.MF.CIT	8.29e-252
c 15	212	8.7	397 40	AQ167755	HS-2196.A1.G10.MF.CIT	2.79e-253
c 16	211	8.7	400 39	AQ124653	HS-2267.B1.H10.MF.CIT	8.29e-253
c 17	213	8.7	405 21	AA935827	om78h06.s1.NCI.CGAP.Ki	9.40e-255
c 18	212	8.7	431 11	AA330549	EST34267 Embryo, 6 wee	2.79e-253
c 19	212	8.7	499 39	AQ140390	HS-3110.B1.A10.T7.CIT	2.79e-253
c 20	213	8.7	593 38	AQ061308	CIT-HSP-2252B20.TF.CIT	9.40e-255
c 21	211	8.7	625 40	AQ275285	RPC1-1.4668SP6.RPC1-1	8.29e-252
c 22	211	8.7	635 38	BI4462	A-916H10.TP.CIT978SK.H	8.29e-252
c 23	211	8.7	635 38	BI4462	CIT-HSP-2009017.TRB.CI	8.29e-252
c 24	212	8.7	640 37	AQ014547	Homo sapiens genomic D	2.79e-253
c 25	211	8.7	701 38	AQ076800	CIT-HSP-2367K11.TF.CIT	8.29e-252
c 26	209	8.6	297 38	BS4826	RPC111-2867.TV.RPC11	7.29e-249
c 27	210	8.6	359 38	AQ002638	CIT978SK-19L16-1.TP.CI	2.46e-250
c 28	209	8.6	420 39	AQ029738	RPC111-41P14.TV.RPC11	7.29e-249
c 29	209	8.6	485 39	AQ139069	HS-3082.B1.C12.MR.CIT	7.29e-249
c 30	209	8.6	487 40	AQ141655	HS-3151.B1.A04.T7.CIT	7.29e-249
c 31	209	8.6	525 38	AQ082123	RPC111-54P4.TV.RPC11	7.29e-249
c 32	210	8.6	589 38	AQ041600	CIT-HSP-2232D19.TF.CIT	2.46e-250
c 33	209	8.6	628 38	BS4637	CIT-HSP-364B14.TR.CIT	7.29e-249
c 34	209	8.6	638 38	BS4637	CIT-HSP-2009017.TRB.CI	8.29e-252
c 35	210	8.6	794 37	BO1721	Homo sapiens chromosome	2.46e-250
c 36	208	8.5	400 29	AQ138601	CSRL-13847-u.CSRL.FLOW	2.46e-250
c 37	208	8.5	400 29	AQ138601	HS-3072.B1.D01.MR.CIT	2.16e-247
c 38	208	8.5	402 39	AQ131159	tr31h02.x1.NCI.CGAP.Pa	2.16e-247
c 39	208	8.5	412 15	C75332	HS-3036.A1.H07.MR.CIT	2.16e-247
c 40	208	8.5	418 27	AI434103	C75332 Human pancreati	2.16e-247
c 41	208	8.5	424 38	AQ058004	LI31b05.x1.NCI.CGAP.Ga	2.16e-247
c 42	208	8.5	457 38	AQ076034	CIT-HSP-234K8.TF.CIT	2.16e-247
c 43	208	8.5	514 38	BS1474	CIT-HSP-2366L4.TF.CIT	2.16e-247
c 44	208	8.5	544 40	AQ171728	CIT978SK-A-61E3.TP.CIT	2.16e-247
c 45	208	8.5	564 38	AQ006837	HS-3172.B2.P08.T7.CIT	2.16e-247
					CIT-HSP-2282B6.TFB.CIT	2.16e-247

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
1	AQ230483	340 bp DNA	AQ230483	AQ230483.1	GI:3655712	human.	Homo sapiens
	HS-2041.B1.B07.MR.CIT	Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-2041 Col-13 Row-D, genomic survey sequence.	AQ230483	AQ230483.1	GI:3655712	human.	Homo sapiens
							Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
							1 (bases 1 to 340)
							Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Furlong,J., Shaker,R., Schmidt,S., Tralcoff,R. and Hood,L.E.
							Construction of a Characterized Clone Resource for Genomic Sequencing
							Unpublished (1998)
							JOURNAL
							COMMENT

Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2041 row: D column: 13
Class: BAC ends
High quality sequence stop: 340.
Location/Qualifiers
1..340
/organism="Homo sapiens"

	/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
	/db_xref="taxon:9606"
	/clone="Plate=2041 Col-13 Row=D"
	/clone_id="CIT Approved Human Genomic Sperm Library D"
	/sex="male"
BASE COUNT	60 a 105 c 71 g 104 t
ORIGIN	
Query Match	9.1%; Score 221; DB 40; Length 340;
Best Local Similarity	86.0%; Pred. No. 1,49e-266;
Matches 257; Conservative	0; Mismatches 42; Indels 0; Gaps 0;
Db	22 TTCCTTTTTCCTTTTGAGACGAGATTTCACCTGTGGTCCCGACGAGCTGCAGATGC 81 2442 ttttttttttttttggacagattgtcttgtaccatcagctgagtgaatgc 2383
Db	82 ACGATCTGGCTCACCAACCTCCGCTCCAGGTTAAAGTATCTCCGCTCAACC 141 2382 gcncttggtccacgaacctcgctcccagaatcaaaatnttcgctcgyc 2323
Db	142 TCCCCAGAGCGGATTACAGCGCATGTGCCACGCGCCACGACTAATTTGATTTT 201 2322 tcctgttaagccaganttacgcccatgctcacacgcgcgctaattngtattnag 2263
Db	202 TAGAGATGGGTTTTCATGTGGTGCAGCGCTGTCTCGAGCTCCCAACTCAGGTATC 261 2262 tagagatgggttcttcacgcttgctcagctgtgcttgaatccccgcgcttagatgc 2203
Db	262 CACCCAGCTCAGCCGCCAAAGTGTGGGATTACAGGCATGAGCCAGCGCGCTGCCA 320 2202 cacccacttggtccccaagaagtgttgaggattacagtgtagccatcgccgtgcga 2144
RESULT	2
LOCUS	A0429198 389 bp DNA GSS 23-MAR-1999
DEFINITION	CITBI-EI-2581D3..TF CITBI-EI Homo sapiens genomic clone 2581D3, genomic survey sequence.
ACCESSION	A0429198
NID	g4496964
VERSION	A0429198.1 GI:4496964
KEYWORDS	GSS.
SOURCE	human. Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 389) Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C. Use of BAC End Sequences from Caltech Libraries for Sequence-Ready Map Building Unpublished (1997)
TITLE	
JOURNAL	
COMMENT	Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hdsel@igrr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/hungen/bac_end_search/Bac_end_search.html . Seq primer: M13-21 Class: BAC ends.
FEATURES	Location/Qualifiers
source	1..389 /organism="Homo sapiens" /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI; Caltech Human BAC Library D" /db_xref="taxon:9606" /clone="2581D3" /clone_id="CITBI-EI"

	BASE COUNT	74 a	114 C	86 g	115 t	/sex="male" /cell_type="sperm"
Query Match						9.1% Score 222; DB 42; Length 389;
Best Local Similarity						85.5%; Pred. No. 4,96e-268;
Matches 260; Conservative						0; Mismatches 44; Indels 0; Gaps 0
Dd	29	TTTTTCTTTTGTGAGACAGATTTTGCTTCCTTTCCCGCAGCGTAGTGCAATGGCG	88			
Cp	2440	tttttttttttttggcagagatttcctctgttacccgagtgaatgcacgtgcgc	2381			
Dd	89	CATCTCACCTACAGGCACACTCCGCCCTCCCGGCTCAAAGCATCTCCGCTGGGCTC	148			
Cp	2380	gntccgggtctaccgcccaacctccctcccacgttacaagnatlntctgccttggtctc	2371			
Dd	149	CTGACTAGCTGSGATTACAGGCATGACACACCACGCGCTAGTAATTTTGTATTTTAA	208			
Cp	2320	ctgagtagcacggnlttaagaacatgcatgcatgacacgccccgactaatltnagta	2261			
Dd	209	CAGACGGGGTTTCTTCATGTTGTGTGACGGCTGCTCGAATCTCCGACCTTAAGTATCA	268			
Cp	2260	gagatagggtttcttccaagtgtgtccaggtctgttctaaccctcgcttatgatcca	2201			
Dd	268	CCTACTCAAGCTCCCGAAGTGCTAAGATTACAGGCGTGAAGCCAGGCGCTGGCGCTGT	328			
Cp	2200	cgcacttgcgtccccaagtgtttgtgattacagtgltgaaacacatcgcttgcgcaaga	2141			
Dd	329	CTTG 332				
Cp	2140	cttg 2137				

FEATURES	Source
RESULT 3	
LOCUS	A0372425 556 bp DNA
DEFINITION	RPC11-143N1.TV RPC11 Homo sapiens genomic clone R-143N1, genomic survey sequence.
ACCESSION	A0372425
NID	94343448
VERSION	A0372425.1
KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 556) Zho,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
TITLE	Use of BAC End Sequences from Library RPC11 for Sequence-Ready Mapping Building
JOURNAL	Unpublished (1997)
COMMENT	Other GSSs: RPC11-143N1..TJ Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbeetlgr.org For clone availability, please contact Pieter de Jong (pieter@dejong.med.buitalo.edu). Clones may be purchased from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html . Seq primer: T7 Class: BAC ends.
FEATURES	Location/Qualifiers
Source	1..556
	/organism="Homo sapiens"
	/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPC11 Human Male BAC Library"
	/db_xref="GDB:7554850"
	/db_xref="taxon:9606"

Best Local Similarity 85.2%; Pred. No. 1,06e-257;
Matches 253; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Db 85 GGCAGGGCCAGTGGCTACGCTGTAATCCACACTTTGGAGCGCGGCGA 144
|||||
Qy 2145 ggcagggcagctgtccacaccttaatcccaacacttggagggcaggtgtgga 2204
|||||
Db 145 TCACCTGAGGTTGGAGTTTGAGACCGCTTACACAGATGAGAAACCCGTGTCTAC 204
|||||
Qy 2205 tcattcaagccggaggttcaagaccagcctgaccacagctggagaacccactctact 2264
|||||
Db 205 AAAAATACGAATTAGCCAGGATGTGGCGCATGCTGTATCCACACTACTACGAGG 264
|||||
Qy 2265 naaatacnaaattagccggcgctgtgagcatgtctgttaanccttgctactcagag 2324
|||||
Db 265 CTGAGCGACGAGAACTGCTTGAACCTGAGAGGTGGAGTGTGAGACAGACGAGC 324
|||||
Qy 2325 ccgagggcagaanaatttcttgaactcgggagagcagaggttcggtgagcccaagncgc 2384
|||||
Db 325 CATTGCCCTCCAGCCCTGGTTACAGAGCGAACTCTGTCTCAGAGAAATAA 381
|||||
Qy 2385 cattgaccctcagccctgggttaacagagcaaaactctgtccaaaaaataaaaaa 2441
|||||

RESULT 8
LOCUS AQ093841 432 bp DNA GSS 26-AUG-1998
DEFINITION HS.3023-B2.G10-T7 CTR Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=20 Row=N, genomic survey sequence.

ACCESSION AQ093841
NID 93465288
VERSION AQ093841.1 GI:3465288
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 432)
Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E. Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors
Unpublished (1997)

JOURNAL COMMENT
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3023 Row: N Column: 20
Class: BAC ends
High quality sequence stop: 432.
Location/Qualifiers
1..432
/organism="Homo sapiens"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
/db_xref="taxon:9606"
/clone_1lb="Plate=3023 Col=20 Row=N"
/clone_1lb="CTR Approved Human Genomic Sperm Library D"
/sex="male"

BASE COUNT 121 a 102 c 120 g 86 t 3 others
ORIGIN

Query Match 8.8%; Score 214; DB 39; Length 432;
Best Local Similarity 84.6%; Pred. No. 3.16e-256;
Matches 252; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Db 37 GGCAGGGCCAGTGGCTACGCTGTAATCCACACTTTGGAGGTCAGAGCTGGCGGA 96

Qy 2145 ggcagggcagctgtgctcaacacttgaatcccaacacttggagggcaggtgtgga 2204
|||||
Db 97 TCACCTGAGTAGGATTGAGATCCAGACAGCCTGACAACTTGGAATCCCATCTCTACT 156
|||||
Qy 2205 tcattcaagccggaggttcaagaccagcctgaccacagctgtggagaacccactctact 2264
|||||
Db 157 AAAAATACGAATTAGCCAGGCGCTGTGTGACATGCTGTATCCACACTACTATGAGG 216
|||||
Qy 2265 naaatacnaaattagccggcgctgtgagcagatgtgtgagctgttaanccttgctactcagag 2324
|||||
Db 217 CTGAGCGAGAGAAATCGCTTGAACCTGNGAGCAGAGTTCGCGTACGCGCATATACGC 276
|||||
Qy 2325 ccgagggcagaanaatttcttgaactcgggagagcagaggttcggtgagcccaagncgc 2384
|||||
Db 277 CATTGCCCTCCAGCCCTGGTTACAGAGCGAACTCTGTCTCAGAGAAATAA 334
|||||
Qy 2385 cattgaccctcagccctgggttaacagagcaaaactctgtccaaaaaataaaaaa 2442
|||||

RESULT 9
LOCUS A1567676 454 bp mRNA EST 26-MAR-1999
DEFINITION trf64p05.x1 NCI CGAP Panl Homo sapiens cdna clone IMAGE:2223057 3' similar to contains Alu repetitive element; mRNA sequence.

ACCESSION A1567676
NID 94526128
VERSION A1567676.1 GI:4526128
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 454)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
TITLE Unpublished (1997)
JOURNAL COMMENT
On Jun 5, 1998 this sequence version replaced gi:3187781.

CONTACT: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/dbp/image/image.html

Seq primer: -400P from Glibco
High quality sequence stop: 409.
Location/Qualifiers
1..454
/organism="Homo sapiens"
/note="Organ: pancreas; Vector: pCW-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT."
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013
/db_xref="taxon:9606"
/map="5q35.3"
/clone="IMAGE:2223057"
/clone_1lb="NCI-CGAP_Panl"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"

BASE COUNT 95 a 121 c 127 g 110 t 1 others
ORIGIN

Query Match 8.8%; Score 215; DB 28; Length 454;
Best Local Similarity 86.9%; Pred. No. 1,06e-257;
Matches 246; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Db 8 GAGTTTCTGTTGGCCAGCGCTGAGATGATGCTGAGCTCGCTCATGCAAC 67
|||||
Cp 2420 gattttgctctgttaccacagctgagtgagtgagcgcgntctggtccacgcacac 2361

Db	68	TCGGCTCCCGAGGTTTCAGACAAATTCCTCCGCTCAGCCTCCGAGTCCGGGATTAAG	127
Cp	2360	tcgctcccccagattccaagaaattntctcgcgcgcctccgcgaagcaaggnlttaacg	2301
Db	128	GCATGCGGCACACGCCCCGGCTAATTTGATTGATTTTATGAGAGATGGGTTCTCCAGT	187
Cp	2300	ccatgctctaccacgcccgcgctaatlttngatltttagtagagatbagggtttctccaagt	2244
Db	188	TGCTCAGGCTGAGTTCGAACCTCCCGACCTTAGGTGATCCGCGCTGCCTCGCCTCCCAAG	247
Cp	2240	tgcctcagctcgtgtcttgaactccgcgctctagtagtaccaccaacctlgtcctcccaag	2181
Db	248	TGCTGAGATTACAGCGCTGAGCCACATCGCGCTGGCGCTCAACATT	290
Cp	2180	tgttctgattacaagctgtgtgagccaacgcgcgtctgtccaagactt	2138

RESULT	10								
LOCUS	AQ347616	516 bp	DNA	GSS	21-JAN-1999				
DEFINITION	RPC111-126024.TV RPC111 Homo sapiens genomic clone R-126024,								
	genomic survey sequence.								
ACCESSION	AQ347616								
NID	94172512								
VERSION	AQ347616.1	GI:4172512							
KEYWORDS	GSS.								
SOURCE	human.								
ORGANISM	Homo sapiens								

REFERENCE
AUTHORS
TITLE

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 516)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
Verter, J. C.
Use of BAC End Sequences from Library RFLII for Sequence-Ready Maps

JOURNAL COMMENT Unpublished (1997)
Other GSSs: RPK111-126024.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
tel: 301.861.2000

Tel.: 301 838 0200
 Fax: 301 838 0208
 Email: hbee@ligr.org
 For clone availability, please contact Pieter de Jong
 (pieter@ligr.med.buffalo.edu). Clones may be purchased from
 Research Genetics (info@resgen.com). BAC end search page:
http://www.ligr.org/cdb/huungen/bac_end_search/bac_end_search.html
 Seq primer: T7
 Class: BAC ends.

FEATURES	Location/Qualifiers
source	1. .516

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/organism="Homo sapiens"
/ntc="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI
RpciII Human Male BAC Library"
/db_xref="GDB:7548359"
/db_xref="taxon:9606"
/clone="R-126024"
/clone_1b="Rpci11"
/sex="Male"
/cell_type="Lymphocytes"
BASE COUNT      102 a      106 c      114 g      194 t
ORIGIN

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Query Match	8.8;	Score 214;	DB 41;	Length 516;
Best Local Similarity	85.1%;	Pred. No. 3.16e-256;		
Matches 252;	Conservative 0;	Mismatches 44;	Indels 0;	Gaps 0;

[illegible]

Db 267 TCTTGGCTCACTGCAACCTCCGGCTCCAGGTTCAGCAATCTCCTGCGCTCAGCCTCCT 326

CP	2378	tcctggctcaacgcgaacacctctgcctcccccaglttccaaatntctcgtcctgcctct	2319
Db	3327	GAGTAGCTGGGATTACAGTCATGCACCAACATGCCGTGGAATTTAGACATTTTAGTGA	386
CP	2318	gagtagcagcagnttaacgcgcacatcgcgtacacagcccgcgtaatttngattttmagtga	2255
Db	387	GATGGGGTTTCTCCATGTTGGTCAGCGCTGATCTTGAACCTCGACCTCGTGATCCCTC	446
CP	2258	gatggggttctccacagtctgtctagcctcgtcttgaaacctcccgcccttagatgatccacc	2199
Db	447	CGCTTGGCCCTCCCAAGTGCTAGGATTACAGTGTCAGCCACTCGCCCGGCCAA	502
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Cp 2258 gatggggttcctccacgttgctcagctgtgtcttgtaactccgcgccttagatgatccacc 2199

Db 447 CGTCTGGCCCTCCCAAAGTGCTAGGATTACAGGTGTGAGCCACTGCGCCCGGCCAA 502

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RESULT 11

LOCUS	AQ377046	623 bp	DNA	GSS	05-MAR-1999
DEFINITION	RPC11-15IM17.TJ RPC11 Homo sapiens genomic clone R-15IM17, genomic survey sequence.				

ACCESSION	AQ377046
NID	94348069
UNIVERSITY	10000000

VERSION AQ3//04b.1 GL:4348069
KEYWORDS GSS.
CONTACT

SOURCE	ORGANISM
human.	Homo sapiens
Rubenstein, Vetterlein, Chaudhary, "Neurobiology of ..."	

Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
AUTHORS
1 (pages 1 to 623)
Zhao, S., Adams, M. D., Nierman, W., Malek, J., de Jong, P. and
T. G.

VENTER, J. C.	Use of BAC End Sequences from Library RPC111 for Sequence-Ready Mapping
---------------	---

JOURNAL
COMMENT
building
Unpublished (1997)
Other_GSSs: RPCI11-151M17.TV

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel.: 301.838.0200

Fax: 301 838 0208
Email: hbeet@tigr.org
For clone availability, please contact Pieter de Jong
(pieterdejong.med.bu@ufl.edu). Clones may be purchased from
Research Genetics (inforesgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: Sp6
Class: BAC ends.

FEAIDRES	Location/Qualifiers
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C	p	2202	caccactctggcctcccacaagtggttgattacagtggtgtagccactgsccttgccaa	2143
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C	p	2142	ga 2141	
R	E	S	RESULT 14	
L	O	C	A0098015 347 bp DNA GSS 26-AUG-1998	
D	E	F	HS_3041_A1_H02_MF_CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone plate=3041 Col=3 Row=O, genomic survey sequence.	
A	C	C	A0098015 g3469044	
N	I	D	A0098015.1 GI:3469044	
K	E	Y	GSS.	
W	O	R	human.	
S	O	U	Homo sapiens	
O	R	G	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;	
R	E	F	Primates; Catarrhini; Hominoidea; Homo.	
A	U	T	1 (bases 1 to 347)	
T	H	E	Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S.,	
A	U	T	Tralcoff,R., Adjajian,C., Blanchard,A., West,A. and Hood,L.E.	
T	H	E	Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors	
J	O	U	Unpublished (1997)	
C	O	M	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel.: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Sequence Tagged Connector Plate: 3041 row: O column: 3 Class: BAC ends High quality sequence stop: 347. Location/Qualifiers 1. 347 /organism="Homo sapiens" /note="Organ: Sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B" /db_xref="taxon:9606" /clone="plate=3041 Col=3 Row=O" /clone_lbp="CIT Approved Human Genomic Sperm Library D" /sex="male"	
F	E	A	FEATURES	
S	O	U	source	
B	A	S	BASE COUNT	
O	R	I	62 a 103 c 80 g 102 t	
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B	E	S	Best Local Similarity 85.0%: Score 211; DB 39; Length 347;	
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D	b	114	GCAATTCGGCTCACCACCACTTCACACTCCAGGTTCCAAGCAATTCTCTGGCTCAGGC 173	
C	p	2382	gcgntctggctcacccagaactctgctctcccaagttcaagnaatttctgctcgccg 2323	
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NID		93561470				
VERSION		AQ167755.1	GI:3561470			
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ORGANISM		Homo sapiens				
REFERENCE		Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS		1 (bases 1 to 397)				
TITLE		Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Furlong,J., Shaker,R., Schmidt,S., Traicoff,R. and Hood,L.E.				
JOURNAL		Construction of a Characterized Clone Resource for Genomic Sequencing				
COMMENT		Unpublished (1998)				
FEATURES						
SOURCE		Contact: Mahairas GG, Wallace JC, Hood L				
		High Throughput Sequencing Center				
		University of Washington				
		401 Queen Anne Avenue North, Seattle, WA 98109, USA				
		Tel: (206) 616-3618				
		Fax: (206) 616-3887				
		Email: jwallace@u.washington.edu				
		Sequence Tagged Connector				
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		Class: BAC ends				
		High quality sequence stop: 397.				
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Dh	112	TGACCTGAGGTGGGAGTTCGAGACGACCGTACCAACATGAGAAACCCGCTCTACT	171			
Qy	2205	tcattcaagccgggaagtcaagaccagcctgaccaacgctgagaaacccatctact	2264			
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Qy	2325	ccgagcgcaanaaatncttgatcagtcggggagcgagagtgctcggtgagccagancgyc	2384			
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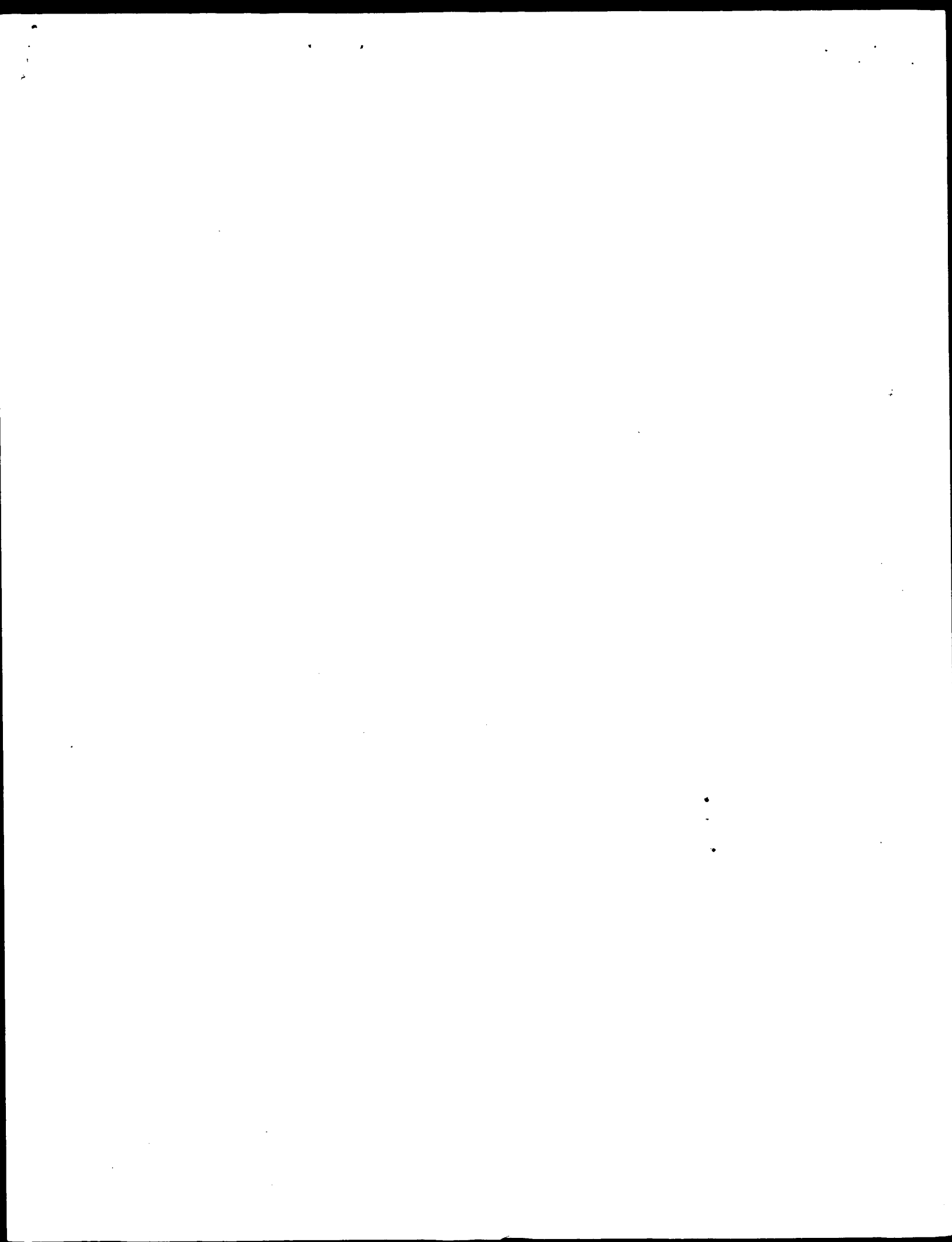
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US-09-246-129-1.rst

Page 9

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Job time : 4186 secs.



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 PD 17-MAY-1996.
 PE 07-NOV-1994; U12880.
 PR 21-NOV-1994; WO-012880.
 PR 21-NOV-1994; ZA-009229.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI N1 J, Rosen CA, Yu G;
 DR WPI; 96-321550/32.
 DR P-PSDB: R99453.
 PR Tumour necrosis factor gamma and corresponding DNA and RNA - for
 PR treating cancer, facilitating wound healing and providing resistance
 PR against infection
 PS A claim 1; Fig 1; 69p; English.
 CC A CDNA clone (T30390), deposited as ATCC 75927, codes for tumour
 CC necrosis factor-gamma (R99453), a novel member of the TNF family. It
 CC was isolated from a human umbilical vein endothelial cell CDNA
 CC library. The coding sequence can be incorporated into a vector and
 CC used for prodn. of recombinant TNF-gamma using bacterial, insect or
 CC mammalian cells as hosts. It may also be used as a diagnostic probe,
 CC for gene mapping, or for the gene therapy of diseases involving
 CC abnormal cellular proliferation, e.g. tumours and cancer. Antisense
 CC sequences are useful as TNF-gamma antagonists.
 SO Sequence 2442 BP; 760 A; 529 C; 511 G; 636 T;
 Query Match 99.8%; Score 2430; DB 21; Length 2442;
 Best Local Similarity 99.9%; Pred. No. 0.00e+00;
 Matches 2439; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DE	Genomic DNA for interferon-gamma production inducer.	
DE	Interferon-gamma; IFN-gamma; production inducer; gene therapy;	
KW	immunocompetent cell; treatment; prevention; malignant tumour;	
KW	viral infection; bacterial infection; immune disease; ds.	
OS	Homo sapiens.	
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FN	EP-816499-A2.	
PD	07-JAN-1998.	
PF	27-JUN-1997; 304616.	
PR	27-JUN-1996; JP-185305.	
PA	(HAYB) HAYASHIBARA SEIBUTSU KAKAKU.	
PI	Kurimoto M, Okura T, Torigoe K;	
DR	WPI; 98-054914/06.	
PT	P-PSDB; W47429.	
PT	Genomic DNA encoding polypeptide inducing interferon-gamma	
PT	production - by immuno-competent cells, useful to treat e.g. human	
PT	malignant tumours or viral diseases.	
PS	Claim 13; Pages 64-73; 74pp; English.	
CC	The present sequence encodes a protein, which induces	
CC	interferon-gamma (IFN-gamma) production in immunocompetent cells.	
CC	The protein has high biological activity, including enhancing	
CC	cytotoxicity of killer cells and inducing killer cell formation,	
CC	in addition to inducing IFN-gamma production by immunocompetent	
CC	cells when expressed in mammalian cells, facilitating its use in	
CC	low dosages to treat/prevent, e.g. malignant tumours, viral or	
CC	bacterial infections and immune diseases. As it is expressed in	
CC	mammalian cells, it also has low toxicity when used in human	
CC	treatments, minimising side effects. The DNA encoding the protein	
CC	can be used in gene therapy, e.g. by injecting vectors containing	
CC	the DNA or transplanting cells.	
SO	Sequence 28994 BP; 9141 A; 5655 C; 5654 G; 8544 T;	
Query Match	9.2%; Score 223; DB 39; Length 28994;	
Best Local Similarity	86.3%; Pred. No. 9,84e-124;	
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QY	2204 atcatctaagcgcggagttcaagccagcctgacacacgcyggaagacccatctac	2263
Db	23548 taaataataaataatagctggcgctgtggcatalagctctgatalcccgctacccggag	23607
QY	2264 taaataataaataatagcggcgctgtggcatalagctctgatalcccgctacccggag	2333
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QY	2324 gccggcgacaggaatcttttaaccgggagcagaggttgcagatggactagatcgtg	2383
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Oy		2384	cattgcaactccagcctgggtgaacaagaacaaacctctgcaccaaaaaaaaaaaaaaa	2442
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AC		Q92779;		
DE		09-DEC-1995	(first entry)	
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KW		Thymopoleitin; diagnostic; therapeutic; gene therapy; ss.		
OS		Homo sapiens.		
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PN		29-JUN-1995.		
PR		13-DEC-1994; U14356.		
PR		21-DEC-1993; US-171382.		
PA	(IMMU-) IMMUNOBIOLOGY RES INST INC.			
PI	Culler MD, Goldstein G, Harris CA, Setcavage DR:			
PI	Shenbagamurthi P, Steklerka JJ, Talle MA,			
DR	WP1: 95-2404/4/31.			
PT	Polynucleotide(s) encoding human thymopoietin proteins - used to			
PT	develop prod. for diagnosis and therapy involving immune or nervous			
PS	system conditions.			
PS	disclosure: Fig 9a-9g; 85pp; English.			
CC	The sequence represents a fragment of the human thymopoietin gene,			
CC	Including exons 4 and 5. DNA encoding human thymopoietin, from			
CC	a cDNA library prepared from human thymus RNA, may be expressed in			
CC	a host cell e.g. bacterium (preferably Escherichia coli), fungus,			
CC	insect or mammalian cell for production of recombinant thymopoietin.			
CC	Thymopoietin has a regulatory effect on the mammalian immune system,			
CC	and can be used for treating/modulating an immune or nervous system			
CC	condition, and for the treatment of chronic infection, autoimmune			
CC	disorders and certain affective psychiatric or neurological			
CC	disorders. The protein and the DNA can be used as diagnostics;			
CC	the DNA can be used in gene therapy.			
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Oy	2265	nnaatatcaaaattagccgggcytgtgtagcgalgctgtaancctgctaactcaga	2324	
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Oy	2325	cggagtcgagaanaattincttaactctgagggagcgaggtttgcgttgacccaan	2384	
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DT		V02032:		
DE		12-JUN-1998	(first entry).	
DE		MAGE-B cluster DNA sequence.		
KW		MAGE-B cluster DNA; testicular seminoma; cancer; screening; leukemia;		

Chr	Gene	Transcript	Location/Qualifiers
OS	Carcioma: ss.		
PH	Homo sapiens.		
FT	Key	3266..7979	
FT	prim_transcript		
FT		/*tag= a	
FT	exon	/label= B2 gene	
FT		3266..3364	
FT		/*tag= b	
FT		/note= "exon 1 of B2 gene"	
FT		3365..6277	
FT		/*tag= c	
FT	intron	/note= "intron 1 of B2 gene"	
FT		6278..7979	
FT		/*tag= d	
FT	exon	/note= "exon 2 of B2 gene"	
FT		6283..7224	
FT		/*tag= e	
FT	CDS	/note= "coding sequence for B2 gene"	
FT		7961..7966	
FT		/*tag= f	
FT	polyA_signal	/note= "polyA signal for B2 gene"	
FT		23546..25194	
FT	exon	/*tag= g	
FT		/note= "exon 1 of B3 gene"	
FT		23607..24647	
FT		/*tag= h	
FT	CDS	/note= "coding sequence for B3 gene"	
FT		25152..25157	
FT		/*tag= i	
FT	polyA_signal	/note= "polyA signal for B3 gene"	
FT		29748..31827	
FT	prim_transcript		
FT		/*tag= j	
FT		/label= B4 gene	
FT	CDS	29808..30848	
FT		/*tag= k	
FT		/note= "coding sequence for B4 gene"	
FT	polyA_signal	31822..31827	
FT		/*tag= l	
FT		/note= "polyA signal for B4 gene"	
FT	prim_transcript	31403..33691	
FT		/*tag= m	
FT		/label= B1 gene	
FT		31403..31474	
FT	exon	/*tag= n	
FT		/note= "exon 1 of B1 gene"	
FT		31475..33957	
FT	intron	/*tag= o	
FT		/note= "intron 1 of B1 gene"	
FT		33958..34062	
FT	exon	/*tag= p	
FT		/note= "exon 2 of B1 gene"	
FT		34063..35056	
FT	intron	/*tag= q	
FT		/note= "intron 2 of B1 gene"	
FT		35057..35139	
FT	exon	/*tag= r	
FT		/note= "exon 3 of B1 gene"	
FT		35140..38087	
FT	intron	/*tag= s	
FT		/note= "intron 3 of B1 gene"	
FT		38088..33691	
FT	exon	/*tag= t	
FT		/note= "exon 4 of B1 gene"	
FT		38148..39191	
FT	CDS	/*tag= u	
FT		/note= "coding sequence for B1 gene"	
FT		33674..33679	
FT		/*tag= v	
FT	polyA_signal	/note= "polyA signal for B1 gene"	
PN	NC09746710-A1.		
PD	11-DEC-1997.		
PE	05-JUN-1997.		
PF	25-APR-1997.		
PR	US-846111.		

PR	05-JUN-1996; US-658578.
PA	(LUDM-) (LUDMIG INSTR CANCER RES.
PI	Boon T, Brassens F, Lurquin C;
PI	WPI: 98-042216/04.
PT	Screening for the possibility of testicular seminoma and other
PT	cancers - using MAGE-Xp gene primers
PS	Claim 7: Pages 22-34; 40pp; English.
CC	This is the MAGE-B cluster DNA sequence. The invention provides a novel
CC	method for screening for the possibility of a testicular seminoma,
CC	non-small cell lung carcinoma, melanoma, breast cancer, sarcoma, or
CC	leukemia in a sample. The method comprises contacting the sample with
CC	at least one nucleic acid molecule which hybridizes to mRNA corresponding
CC	to an MAGE-Xp gene, and determining hybridisation as a determination of
CC	possible presence of testicular seminoma, non-small cell lung carcinoma
CC	melanoma, breast cancer, sarcoma, or leukemia in the sample. By assaying
CC	for the MAGE-B1 gene, or MAGE-B2 gene, both contained within this 40352
CC	base pair MAGE-B cluster DNA sequence, the presence of such cancers in a
CC	sample can be determined. The genomic DNA that encodes the MAGE-B2 gene
CC	consists of nucleotides 3265-7979 of this MAGE-B cluster DNA sequence.
CC	The nucleic acid molecule that encodes a MAGE-B1 gene, consists of, in
CC	5' to 3' order, nucleotides 31403-31474, 33958-34062, 35057-35139, and
CC	38088-39691, nucleotides 31403-31474, 33958-34062, and 38088-39691,
CC	nucleotides 35057-35139 and 38088-39691, and nucleotides 33958-34062 and
CC	38088-39691 of this sequence. The primers specific for the MAGE-B
CC	gene can be used in a kit to amplify a MAGE-B gene.
CC	Sequence 40352 BP; 11599 A; 8654 C; 9772 G; 10327 T;
SO	
Query Match	8.8%; Score 214; DB 40; Length 40352;
Best Local Similarity	85.1%; Pred. No. 9.21e-118;
Matches	258; Conservative 0; Mismatches 44; Indels 1; Gaps 1;
Db	8059 tctcagccgaggttcagttgtctacatctgttaacctccagcattggagagctgagttg 8118
Qy	2141 tcttgcgcagcagcgagtgctcacacctgttaa-tcccaacctttggagggccaagtgg 2199
Db	8119 gtggtatcacttgagtgctggagagtttcgagaccagccttgacaaatggagaaacctgtct 8178
Qy	2200 gtggatcatctaaagccgggaggttcaagaccagccttccacaaatgtagaaccacctct 2259
Db	8179 ctactaaataatacaaaatttagccagcgctgtgtgacgatgtcgttaatgacgactactg 8238
Qy	2260 ctactnaaaaatacnaaaatttgcggcgctgtgttgcgcattgctgttaacctgtactca 2319
Db	8239 ggaagctcaagcagagagatcacttgaaccacagagagcgagagttgctgtgaacgcagac 8298
Qy	2320 ggaagccgagcagaanaatttcttgaactcggggagcagaggttgcgtgagcccgagc 2379
Db	8299 tgcgcacttgcactccagccttgggcaacaaagacggaactcctcttaaaaaaaaaa 8358
Qy	2380 cgcgcacttgcactccagccttgggtaacaaagacaaactcttccaaaaaaaaaaaaa 2439
Db	8359 aaa 8361
Qy	2440 aaa 2442
RESULT	
ID	6
AC	T61677 standard; DNA: 8174 BP.
DE	19-JUN-1997 (first entry)
DE	Human alpha(1,2)-lucosyltransferase DNA.
KW	Alpha(1,2)-lucosyltransferase; glycosylation; oligosaccharide;
KW	blood group H; ss.
OS	Homo sapiens.
FT	Key
FT	Location/Qualifiers
FT	cds 4686..5783
FT	cds /*tag= a
PN	WO9709421-A1.
PD	13-MAR-1997.
PF	06-SEP-1996; U13816.
PR	08-SEP-1995; US-552058.
PA	(UNMI) UNIT MICHIGAN.
PI	Legault DJ, Lowe JB;

DR WPI: 97-192897/17.
 P-PSDB: M13640.
 PT New recombinant fucosyltransferase proteins - useful for modifying cell surface oligosaccharide structures
 PS Example 1; Page 274-279; 329pp; English.
 CC A DNA sequence (761677) codes for human GDP-Fuc-beta-D-galactoside alpha(1,2)-fucosyltransferase (M13640), an enzyme involved in the expression of type I and II blood group H structures. It was obtained by transfecting mouse L cells with DNA derived from human A431 cells, and selection of transfectants that expressed the H antigen by using anti-H antibody in a panning procedure. The DNA can be used to construct animal cell lines with specific capabilities with respect to post-translational modification of the oligosaccharides of expressed proteins or lipids, or to produce recombinant enzyme for use in CC oligosaccharide prodn.
 SQ Sequence 8174 BP; 1628 A; 2229 C; 2322 G; 1995 T;
 Query Match 8.7%; Score 212; DB 29; Length 8174;
 Best Local Similarity 84.8%; Pred. No. 1.95e-116;
 Matches 251; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
 Db 4002 ttatttttttttgagagagagatttcaactctgttgcacagctgagtgatggcat 4061
 Cp 2440 ttttttttttttgagagagagatttgcctgttaccagctgagtgatggcatg 2381
 Db 4062 gatctagctacacgaactcccgcccgaggttcagcgattctcctgctcagcctc 4121
 Cp 2380 gntctgggtctacacgaactcccgcccgaggttcagcgattctcctgctcagcctc 2321
 Db 4122 ccgagtgctggagattacagcagcgcacacatcgccgagtaatttgaatga 4181
 Cp 2320 ctgagtagcagcaggttacagcagcgcacacgctgagtaatttgaatga 2261
 Db 4182 gaacacgggttttccagctgtgtcagctgtgtcgaactcccaacccagtgatca 4241
 Cp 2260 gagatgggttttccagctgtgtcagctgtgtcgaactcccaacccagtgatca 2201
 Db 4242 ccacacttgctccccaagtgctggattacagtgtagcagcagcgctggcc 4297
 Cp 2200 ccacacttgctccccaagtgctggattacagtgtagcagcagcgctggcc 2145
 RESULT 7
 ID 013332 standard; DNA; 8174 BP.
 AC 013332;
 DT 07-NOV-1991 (first entry)
 DE GDP-Fuc:beta-D-galactoside alpha(1,2)-fucosyltransferase gene.
 KW Glycosyltransferase.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT cds 4686..5783
 FT /*tag= a
 PN WO9112340-A.
 PD 22-AUG-1991.
 PF 14-FEB-1991; 000899.
 PR 14-FEB-1990; US-480133.
 PR 14-FEB-1990; US-479858.
 PR 12-DEC-1990; US-627621.
 PA (UNMT) UNIV OF MICHIGAN.
 PI Lowe JB;
 DR WPI: 91-267151/36.
 DR P-PSDB: R13751.
 PT Isolation of gene conveying post-translational characteristic - e.g. the presence of soluble or membrane bound oligo or PT polyaccharide or glycosyltransferase.
 PS Disclosure; Fig 3; 15pp; English.
 CC The DNA encodes a protein sequence capable of functioning as a GDP-Fuc:beta-D-gal alpha(1,2)-fucosyltransferase. The sequence coded by nucleotides 4782 - 5780 represents the functional protein.
 CC The enzyme produced by the DNA sequence can be used in enzymatic fucosylation of chain-terminating galactose residues on lactose-amine or neolacto type beta-D-galactoside to alpha-2-L-fucose

CC residues. See also 013330-013333.
 SQ Sequence 8174 BP; 1628 A; 2229 C; 2322 G; 1995 T;
 Query Match 8.7%; Score 212; DB 2; Length 8174;
 Best Local Similarity 84.8%; Pred. No. 1.95e-116;
 Matches 251; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
 Db 4002 ttatttttttttgagagagagatttcaactctgttgcacagctgagtgatggcat 4061
 Cp 2440 ttttttttttttgagagagagatttgcctgttaccagctgagtgatggcatg 2381
 Db 4062 gatctagctacacgaactcccgcccgaggttcagcgattctcctgctcagcctc 4121
 Cp 2380 gntctgggtctacacgaactcccgcccgaggttcagcgattctcctgctcagcctc 2321
 Db 4122 ccgagtgctggagattacagcagcgcacacatcgccgagtaatttgaatga 4181
 Cp 2320 ctgagtagcagcaggttacagcagcgcacacgctgagtaatttgaatga 2261
 Db 4182 gaacacgggttttccagctgtgtcagctgtgtcgaactcccaacccagtgatca 4241
 Cp 2260 gagatgggttttccagctgtgtcagctgtgtcgaactcccaacccagtgatca 2201
 Db 4242 ccacacttgctccccaagtgctggattacagtgtagcagcagcgctggcc 4297
 Cp 2200 ccacacttgctccccaagtgctggattacagtgtagcagcagcgctggcc 2145
 RESULT 8
 ID 056908 standard; DNA; 8174 BP.
 AC 056908;
 DT 26-JUL-1994 (first entry)
 DE DNA encoding a glycosyltransferase.
 KW Glycosyltransferase; fucosyltransferase; GDP-Fuc; in vitro; cell;
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT cds 4686..5783
 FT /*tag= a
 PN WO9402616-A.
 PD 03-FEB-1994.
 PF 20-JUL-1993; 006703.
 PR 20-JUL-1992; US-914281.
 PA (UNMT) UNIV MICHIGAN.
 PI Lowe JB;
 DR WPI: 94-048874/06.
 DR P-PSDB: R45936.
 PT DNA fragment encoding a glycosyltransferase - can be used for in vitro reactions to modify cell surface oligosaccharides e.g. blood gp. determinants, to protect against transplant rejection
 PS Disclosure; Fig 3; 249pp; English.
 CC The sequence is that encoding human glycosyl transferase. The enzyme produced by the DNA may be non glycosylated. This prevents premature loss of enzyme activity. It can also be used in in vitro reactions to modify cell surface oligosaccharide mols. e.g. blood group determinants.
 CC See also 056905-12.
 SQ Sequence 8174 BP; 1628 A; 2228 C; 2322 G; 1996 T;
 Query Match 8.7%; Score 212; DB 9; Length 8174;
 Best Local Similarity 84.8%; Pred. No. 1.95e-116;
 Matches 251; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
 Db 4002 ttatttttttttgagagagagatttcaactctgttgcacagctgagtgatggcat 4061
 Cp 2440 ttttttttttttgagagagagatttgcctgttaccagctgagtgatggcatg 2381
 Db 4062 gatctagctacacgaactcccgcccgaggttcagcgattctcctgctcagcctc 4121
 Cp 2380 gntctgggtctacacgaactcccgcccgaggttcagcgattctcctgctcagcctc 2321
 Db 4122 ccgagtgctggagattacagcagcgcacacatcgccgagtaatttgaatga 4181
 Cp 2320 ctgagtagcagcaggttacagcagcgcacacgctgagtaatttgaatga 2261
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BASE COUNT 854 a 603 c 577 g 750 t 1 others
ORIGIN

Query Match 98.2%; Score 2393; DB 31; Length 2785;
Best Local Similarity 99.1%; Pred. No. 0.00e+00;
Matches 2423; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

Db 340 CCAAAATCAGAGAAATTCATCTACTATTCACAGTTGGCCAACTTCCAGTCAAGTACAGAGA 399
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Db 460 GACAGTGCAGAAAGATATTTAGAACCCCTAAAACCTAGAGTTAAAAAGAGAGAT 519
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Db 580 ATTGGTGTATCATTTGACTTAAGAGAAATTTTGTGGTGAAGCTCTGAGTGAAGATTAG 639
QY 241 attggtgtatacttctgactaagaagaatatttctgtgtgagccctgagtgagattag 300
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QY 539 ataggggattccttaaccttacttctgtctccagagatcagatcagataaattaa 598
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Db 1000 TCCAAGATGTTATCTTCTTGAACAAGTGTATGTCGACATATTTCTTCAATTTCT 1059
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Db 1060 CTTCCCAAGAGAGTTTATAGTGTATGATTTGATTCAGTCACTTATAGTTTGAAGA 1119
QY 719 cttcccaagaagagctttagtctgtagtatattcgacactttagtctatttgagaaa 778
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QY 779 tgatatagagcgctttttaaagcaagctacagtttccaatgagaaaaatlaactctct 838
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Db 2319 TATTCAGTAGAGTTTCTTGGCCACCTAATTTGTGCTGGGTTCTACCTTAACCCAGAGA 2378

variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above.

This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre chromosome X mapping group. Further information can be found at <http://www.sanger.ac.uk/HGP/chrX/>

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unseq' feature key.

The true left end of clone 196E23 is at 1 in this sequence. The true right end of clone 196E23 is at 123004.

196E23 is from the library RPCI1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.

For further details see <http://Dacpac.med.buffalo.edu/>.

FEATURES

SOURCE

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evidence=not_experimental
complement(join(17975..18063,23693..23768))
/gene="dJ196E23.1"
/note="isoform 2: match: protein Q99991"
/codon_start=1
evidence=not_experimental
/protein_id="CAB10728.1"
/db_xref="PID:e1240252"
/db_xref="PID:g2808419"
/db_xref="GI:2808419"
/db_xref="SPTRMBL:Q99991"
/translacion="MFSSFLDKRLVYSGSASTSLPNETLSELETPGKYSILPPNHM
GPHRYLOHL"
complement(join(17975..18063,23693..23746,25506..25925,
38280..38493))
/gene="dJ196E23.1"
/note="isoform 1: match: protein Q99990"
/codon_start=1
evidence=not_experimental
/protein_id="CAB10728.1"
/db_xref="PID:e1240251"
/db_xref="PID:g2808418"
/db_xref="GI:2808418"
/translacion="MEMKKTALRLPKGOKPIKTEENSRVCLFTYPOGDISSVDEH
FSRALSNKSPQELTPSSQSGVMLKDDSGSPQWRYSBPWKPOEVEVTNNAAC
NLAVGPMVAVQFSPSLARASVYGLMHPSSILAGSSLEPGSHFPRARHLVPEQ
PDGKREPLSLLOODRCLARQDSAAENKNGPGIAGSTGLTLPFGSVHYKLYVS
RGSASTSLPNETLSELETPGKYSILPPNHMGPRLYLOHL"
20396..20484
/note="MIR2 repeat: matches 14..103 of consensus"
20903..21206
/note="AluSP repeat: matches 1..303 of consensus"
21750..21845
/note="MIR repeat: matches 57..153 of consensus"
22387..22488
/note="MIR2 repeat: matches 146..21 of consensus"
22584..22714
/note="F1AM_C repeat: matches 131..2 of consensus"
22819..23010
/note="MIR repeat: matches 231..47 of consensus"
23162..23433
/note="2 copies of 136 mer 95 & conserved"
24111..24152
/note="MIR2 repeat: matches 97..138 of consensus"
26214..26515
/note="AluX repeat: matches 1..302 of consensus"

```



```

DEFINITION      Homo sapiens BAC clone 215012 NG35, NG36, G9A, NG22, G9, HSP70-2,
                  HSP70-1, HSP70-HOM, snRNP, G7A, NG37, NG23, and MutsH5 genes,
                  complete cds.
ACCESSION       AF134726
NID             94529886
VERSION         AF134726.1  GI:4529886
KEYWORDS
SOURCE          human.
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1 (bases 1 to 180283)
AUTHORS         Rowen,L., Qin,S., Madan,A., Dickhoff,R., Dors,M., Madan,A.,
                Hicks,P., Loretz,C., Ratcliffe,A., Abbasi,N., Shaffer,T. and
                Hood,L.
TITLE           Sequence of the human major histocompatibility complex class III
                region
JOURNAL         Unpublished
REFERENCE       2 (bases 1 to 180283)
AUTHORS         Rowen,L.
TITLE           Direct Submission
JOURNAL         Submitted (15-MAR-1999) Department of Molecular Biotechnology, Box
                357730 University of Washington, Seattle, WA 98195, USA
COMMENT         Sequencing methodology: high redundancy shotgun in plasmids.
                Interspersed Repeats were identified with RepeatMasker (available
                from http://ftp.genome.washington.edu/RM/RepeatMasker.html). This
                sequence overlaps cosmid S22A (AF019413) by 2363 bases and BAC
                210G24 (AF129756) by 12177 bases.
                Location/Qualifiers
FEATURES
  source         1..180283
                 /organism="Homo sapiens"
                 /db_xref="taxon:9606"
                 /clone="BAC 215012"
                 /map="6p21.3"
                 /chromosome="6"
                 /note="major histocompatibility complex class III region"
  misc_feature   1..2363
                 /note="Overlap span with cosmid S22A in AF019413."
  repeat_region complement(103..402)
                 /rpt_type=dispersed
                 /rpt_family="AluSx"
  variation      408..409
                 /note="cosmid S22A: ttct; BAC 215012: tt"
                 /replace="ttct"
                 /complement(420..480)
  repeat_region /rpt_type=dispersed
                 /rpt_family="L1PA16"
                 /complement(458..732)
  repeat_region /rpt_type=dispersed
                 /rpt_family="L1PA13"
                 /complement(834..1134)
                 /rpt_type=dispersed
                 /rpt_family="AluSx"
  variation      1134..1136
                 /note="cosmid S22A: ct; BAC 215012: ctt"
                 /replace="ct"
                 /complement(1139..1257)
  repeat_region /rpt_type=dispersed
                 /rpt_family="AluSg1"
                 /complement(1446..1746)
  variation      1445..1446
                 /note="cosmid S22A: ctt; BAC 215012: ct"
                 /replace="ctt"
                 /complement(1446..1746)
  repeat_region /rpt_type=dispersed
                 /rpt_family="AluSx"
                 /complement(1843..2430)
  variation      1843
                 /note="cosmid S22A: t; BAC 215012: c"
                 /replace="t"
                 /complement(2430..2489)
  repeat_region /rpt_type=dispersed
                 /rpt_family="MLT1A2"
                 /complement(2831..2884)

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/rpt_type=dispersed
/rpt_family="LINE2"
complement(3091..3392)
/rpt_type=dispersed
/rpt_family="AluY"
complement(3416..3712)
/rpt_type=dispersed
/rpt_family="AluSg"
complement(3719..3790)
/rpt_type=dispersed
/rpt_family="MLT2FA"
3813..4084
/rpt_type=dispersed
/rpt_family="AluSg"
4086..4375
/rpt_type=dispersed
/rpt_family="AluSg"
complement(4417..4729)
/rpt_type=dispersed
/rpt_family="AluSg"
4781..4910
/rpt_type=dispersed
/rpt_family="FLAM_A"
complement(4939..4968)
/rpt_type=dispersed
/rpt_family="MLT2E"
complement(4980..5112)
/rpt_type=dispersed
/rpt_family="AluUb"
complement(5167..5468)
/rpt_type=dispersed
/rpt_family="AluSx"
complement(5607..5738)
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/rpt_family="LINE2"
5786..5873
/rpt_type=dispersed
/rpt_family="L1ME3A"
5885..5938
/rpt_type=dispersed
/rpt_family="MER5A"
5955..6090
/rpt_type=dispersed
/rpt_family="FLAM_C"
6099..6389
/rpt_type=dispersed
/rpt_family="AluSx"
6403..6446
/rpt_type=dispersed
/rpt_family="MER5A"
complement(6711..7011)
/rpt_type=dispersed
/rpt_family="AluSx"
complement(7029..7330)
/rpt_type=dispersed
/rpt_family="AluSx"
7486..7688
/rpt_type=dispersed
/rpt_family="AluUb"
7689..7851
/rpt_type=dispersed
/rpt_family="L1MB8"
7852..8150
/rpt_type=dispersed
/rpt_family="AluSg"
8151..8263
/rpt_type=dispersed
/rpt_family="L1MB6"
8290..8425
/rpt_type=dispersed
/rpt_family="FLAM_C"
8451..8730
/rpt_type=dispersed

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repeat_region      /rpt_family="AluJb"
                   8737..8839
                   /rpt_type=dispersed
                   /rpt_family="L1MB5"
repeat_region      8816..8972
                   /rpt_type=dispersed
                   /rpt_family="L1ME3"
repeat_region      complement(9034..9357)
                   /rpt_type=dispersed
                   /rpt_family="TIGGEK1"
repeat_region      complement(9358..9659)
                   /rpt_type=dispersed
                   /rpt_family="AluXs"
repeat_region      complement(9662..9735)
                   /rpt_type=dispersed
                   /rpt_family="TIGGEK1"
repeat_region      9736..9882
                   /rpt_type=dispersed
                   /rpt_family="FLAM_C"
repeat_region      9884..10185
                   /rpt_type=dispersed
                   /rpt_family="AluSq"
repeat_region      10189..10351
                   /rpt_type=dispersed
                   /rpt_family="AluSc"
repeat_region      10357..10419
                   /rpt_type=dispersed
                   /rpt_family="AluJb"
repeat_region      complement(10427..10711)
                   /rpt_type=dispersed
                   /rpt_family="AluJb"
repeat_region      complement(10871..11176)
                   /rpt_type=dispersed
                   /rpt_family="AluSq"
repeat_region      complement(12410..12541)
                   /rpt_type=dispersed
                   /rpt_family="FLAM_C"
repeat_region      complement(12577..12873)
                   /rpt_type=dispersed
                   /rpt_family="AluJb"
repeat_region      13413..13701
                   /rpt_type=dispersed
                   /rpt_family="AluSq"
repeat_region      13702..13744
                   /rpt_family="AT_rich"
repeat_region      complement(13907..13948)
                   /rpt_type=dispersed
                   /rpt_family="MIR"
repeat_region      complement(13995..14046)
                   /rpt_type=dispersed
                   /rpt_family="ME57B"
repeat_region      complement(14378..14674)
                   /rpt_type=dispersed

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Note: remainder of annotations omitted.

Query Match	9.5%	Score 231;	DB 31;	Length 180283;
-------------	------	------------	--------	----------------

Matches	263;	Conservative	0;	Mismatches	38;	Indels	0;	Gaps	0
---------	------	--------------	----	------------	-----	--------	----	------	---

Db 85384 TTTT TTTT TTGAGACAGAGTTCCGCTCTGTGGCCAGGCTGGAGTGCAATGGC 85443

Cp 2442 ttttttttttttgacagagtcttgctcttgttaccagctggagtgcattgac 2383

Db 85444 GCGATCTGGCTCACAGCAACCTCCGCCCTCCAGGTTCAAGCCATTCTCCTGCTCAGCC 85503

CP 2382 gcgntctgggtcaccgcaacctctgcctcccaagtccaagnaatnttctgcctcgcc 2323

Db 85504 TCCAGGGTAGCTGGGATTACAGGCATGCGCCACCACACCCGGCTAATTGTATTTTAA 85563

Cp 2322 tcctgagtagccagnttacagccatgcgtaccacgcccgcgtaattngtatttnag 2263

Db 85564 TAGAGATGGGGTTTCTCCATGTTGGTCAGGCTGGTCTCGAAGTCCAGACCTCAGGTGATC 855623

Cp 2262 tagagatagggggtttcttcacagcttgcacagtcgctgttaactcccgagccttagatgac 2203
 |||||
 Db 8564 CGCCCCCTCGGCTCCCAAGTCGTGGGATATATAGTGTATGACCAACCGCCCTCGGCTA 8568
 |||||
 Cp 2202 caccacacttgcctcccaagaagtgtgattacagttgtgacacatcgccctgagcaca 2143
 |||||
 Db 85684 G 85684
 Cp 2142 g 2142

RESULT	6			
LOCUS	HS625H18	185371 bp	DNA	PRI 11-DEC-1998
DEFINITION	Human DNA sequence from clone 625H18 on chromosome 6p22.2-23.			

GSSs and putative CpG islands, complete sequence.

NID 93676217

KEYWORDS HTG; CpG island; Helix-loop-helix; ID4; human

ORGANISM

REFERENCE 1 (bases 1 to 185371)
Primates; Catarrhini; Hominoidea; Homo.

AUTHORS Masahigshi-Morimatsu, M
TITLE Direct Submission

JOURNAL
 SUBMITTED (08-DEC-1998) sanger center, hinxton, cambridgeshire
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk clone

On Sep 30, 1998 this sequence version replaced q1:3646106.

Where differences are found these are annotated as variations

variation annotation may not be found in the sequence submission

only a small overlap as described above.

end of clone 498I24 (AL031057) is at 51918 in this sequence.

as follows. An attempt is made to resolve all sequencing problems,

annotated human repeat sequence elements (e.g. Alu). Where the

feature key.

human chromosome 6, constructed by the Sanger Centre Chromosome 6 Working Group. Further information can be found at

<http://www.sanger.ac.uk/HGF/chr6>
635H19 is from the library BPC14 constructed at the Roswell Park

details see <http://hacpac.med.buffalo.edu/VECTOR>: ncypac?

FEATURES	LOCATION/QUALITERS
COURSE	1 185371

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/organism="Homo sapiens"
/db xref="taxon:9606"
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```
/c]one="625H18"
```

```
/llap= pzz:z-zz
/clone 1th="BPCTA"
```

```
variation
239: .201
/note="c]one 498T24: gac in this entry: substitution"
```

```
repeat region      /replace- gcc
711. 758
```

variation 2117. .2119 /MOCE- DZ IEPeac. machines 2000. .2/00 01 CONDENSAS

```
/proc/cmdline root=/dev/mmcblk0p1 rw noinitramfs  
/replace="tcq"
```

```

/clone 498I24; cat in this entry; substitution"

```


[illegible]

Cp	2202	caccaccttgctccccaagtgttggaattacaggtgtagcaccatcgccgcctggcc	2145
RESULT	9		
LOCUS	HS302D9	145871 bp	DNA PRI 24-NOV-1998
DEFINITION	Human DNA sequence from PAC 302D9 on chromosome 22q11.2-qter. Contains STS, complete sequence.		
ACCESSION	Z82198		
NID	93164067		
VERSION	282198.1	GI:3164067	
KEYWORDS	HTG.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 145871)		
AUTHORS	Bridgeman,A.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-JUL-1997) E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On May 28, 1998 this sequence version replaced gi:1772948. IMPORTANT: This sequence is the entire insert of clone 302D9. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap. This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre chromosome 22 mapping group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22/ This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The true left end of clone 302D9 is at 1 in this sequence. The true right end of clone 41562 is at 35164. The true left end of clone 282F2 is at 69679. The true right end of clone 302D9 is at 145871. 302D9 is from the library RPcll constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/. Location/Qualifiers 1..145871 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="22" /map="q11.2-qter" /clone="302D9" /cclone_id="RPcll" 188..244 /note="MER3 repeat: matches 209..155 of consensus" 246..561 /note="Alusx repeat: matches 1..302 of consensus" 585..759 /note="MER3 repeat: matches 166..1 of consensus" 889..933 /note="MER5A repeat: matches 71..26 of consensus" 1029..1336 /note="Alusp repeat: matches 303..1 of consensus" 1446..1583 /note="MIR repeat: matches 20..160 of consensus" 2359..2659 /note="Alusc repeat: matches 299..3 of consensus" 2679..2980 /note="Alusq repeat: matches 302..2 of consensus" 3344..3643 /note="Aluy repeat: matches 2..301 of consensus" 3747..3922 /note="MIRle repeat: matches 188..365 of consensus" 3926..4275		
FEATURES	source		


```

repeat_region /chromosome="22"
               /clone="821D11"
               /map="q12.3-13.1"
               /clone.lib="RPC15"
               complement(445..743)
               /note="Aluub repeat: matches 302. .8 of consensus"
               446..448
               /note="clone 10966; tct in this entry; substitution"
               /replace="ttt"
               join(1230..1711,13695..>13736)
               /gene="dJ821D11.1"
               /note="this gene and dJ821D11.2 could be part of one gene;
               match: ESTs AA19437 AA332515"
               /evidence="not_experimental"
               /product="dJ821D11.1 (PUTATIVE protein)"
               1230..13736
               /gene="dJ821D11.1"
               1314..1316
               /gene="dJ821D11.1"
               /note="clone 10966; tgt in this entry; substitution"
               /replace="tct"
               join(1601..1711,13695..>13736)
               /gene="dJ821D11.1"
               /note="other possible startcodon at 1583"
               /codon_start=1
               /evidence="not_experimental"
               /product="dJ821D11.1 (PUTATIVE protein)"
               /protein_id="CA16279.1"
               /db_xref="PID:94200330"
               /db_xref="GI:4200330"
               /translation="MLALTLAKADSPRTALCSNMLTASFSAQHQKSLQDKPLLSQ
               ACVGCLE"
               1760..1762
               /gene="dJ821D11.1"
               /note="clone 10966; gag in this entry; substitution"
               /replace="ggg"
               1773..1895
               /note="MIR repeat: matches 47. .182 of consensus"
               1901..1903
               /gene="dJ821D11.1"
               /note="clone 10966; tca in this entry; substitution"
               /replace="tta"
               2302..2304
               /gene="dJ821D11.1"
               /note="clone 10966; gga in this entry; substitution"
               /replace="gaa"
               complement(3042..3133)
               /note="LIMC1 repeat: matches 1079. .988 of consensus"
               complement(3162..3456)
               /note="AluSP repeat: matches 297. .2 of consensus"
               complement(3457..3551)
               /note="MIR repeat: matches 149. .59 of consensus"
               complement(3552..3847)
               /note="Aluub repeat: matches 299. .2 of consensus"
               4753..4754
               /gene="dJ821D11.1"
               /note="clone 10966; tt in this entry; deletion"
               /replace="ttgagt"
               4791..4792
               /gene="dJ821D11.1"
               /note="clone 10966; tt in this entry; deletion"
               /replace="ttattatt"
               complement(4800..5089)
               /note="AluSg repeat: matches 303. .2 of consensus"
               5107..5112
               /gene="dJ821D11.1"
               /note="clone 10966; tttat in this entry; insertion"
               /replace="ttt"
               complement(5128..5427)
               /note="AluY repeat: matches 300. .1 of consensus"
               5359..5361
               /gene="dJ821D11.1"

variation
repeat_region /note="clone 10966; att in this entry; substitution"
               /replace="act"
               complement(5430..5729)
               /note="AluSg repeat: matches 300. .1 of consensus"
               5730..5775
               /note="23 copies 2 mer tt 87% conserved"
               5761..5762
               /gene="dJ821D11.1"
               /note="clone 10966; at in this entry; deletion"
               /replace="att"
               5772..5773
               /gene="dJ821D11.1"
               /note="clone 10966; tt in this entry; deletion"
               /replace="tat"
               complement(5777..6075)
               /note="AluY repeat: matches 299. .1 of consensus"
               5778..5779
               /gene="dJ821D11.1"
               /note="clone 10966; tt in this entry; deletion"
               /replace="ttat"
               5780..5782
               /gene="dJ821D11.1"
               /note="clone 10966; tat in this entry; substitution"
               /replace="ttt"
               5799..5801
               /gene="dJ821D11.1"
               /note="clone 10966; cgg in this entry; substitution"
               /replace="cag"
               5868..5870
               /gene="dJ821D11.1"
               /note="clone 10966; ccg in this entry; substitution"
               /replace="ctg"
               complement(6080..6211)
               /note="FLAM_C repeat: matches 133. .1 of consensus"
               6432..6434
               /gene="dJ821D11.1"
               /note="clone 10966; atg in this entry; substitution"
               /replace="agg"
               complement(7157..7269)
               /note="MER42c repeat: matches 1538. .1419 of consensus"
               7588..7653
               /note="MIR2 repeat: matches 79. .145 of consensus"
               7748..7789
               /note="MER46 repeat: matches 88. .232 of consensus"
               complement(7895..8177)
               /note="AluSx repeat: matches 302. .18 of consensus"
               complement(8307..8606)
               /note="AluSx repeat: matches 300. .1 of consensus"
               complement(8708..8887)
               /note="Aluub repeat: matches 297. .117 of consensus"
               8898..9197
               /note="AluSx repeat: matches 1. .302 of consensus"
               9047..9049
               /gene="dJ821D11.1"
               /note="clone 10966; gcg in this entry; substitution"
               /replace="gtg"
               complement(9207..9329)
               /note="Aluud repeat: matches 123. .1 of consensus"
               complement(9330..9609)
               /note="LIMB3 repeat: matches 930. .640 of consensus"
               complement(9948..10250)
               /note="AluSx repeat: matches 301. .1 of consensus"
               complement(10457..10754)
               /note="AluSg repeat: matches 300. .1 of consensus"
               10699..10701
               /gene="dJ821D11.1"
               /note="clone 10966; cgc in this entry; substitution"
               /replace="cac"
               10876..10878
               /gene="dJ821D11.1"
               /note="clone 10966; ccg in this entry; substitution"
               /replace="ctg"
               10969..10971

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/gene="d3821D11.1"
/note="clone 10966; ggc in this entry; insertion"
/replace="gc"

*** remainder of annotations omitted.

Query Match 9.2%; Score 223; DB 29; Length 76727;

Best Local Similarity 87.8%; Pred. No. 9,48e-147;

Matches 232; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Db 57454 GTGGCTCACACCTAATCCAGACATTTGGAGCGCGGATGATCAGTGTAGT 57513

QY 2156 gtggctcacacctgtaacacacacttgaggccaaagtgtggtgacatacctgaagc 2215

Db 57514 TGGAGTTTGAGACACCTGACACACATGAGAGAAACCCGCTGTACTTAAATAATCAAA 57573

QY 2216 cggaggttcaagacagcctgacacacgttgagaacacccactctactnaaatatcnaa 2275

Db 57574 ATTGCGCGGCGCTGTGGACATGCTGTATCCACTCTAGAGAGGTAGGACAGGA 57633

QY 2276 attagccggtgtgtgtgacatgctgtancttgctactaagagagcgcagagaa 2335

Db 57634 GAATTGCTTAACCCGAGGAGAGAGTTCAGTGAAGCCGAGATCGCGCATTCGACTCC 57693

QY 2336 naatttctgaactggtggaagcagaggttcggtgagccagangcgcacattgcactcc 2395

Db 57694 AGCCTGGGCAACAGACAGACTGTCTCAAAAAA 57740

QY 2396 agcctggttaacagagcaactctgtccaaaaa 2442

RESULT 12
LOCUS HS469D22 85285 bp DNA HTG 16-MAR-1999
DEFINITION Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone
ACCESSION AL031284
NID 94455561
VERSION AL031284.2 GI:4455561
KEYWORDS HTG; HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 85285)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-1999) Wellcome Trust Genome Camps, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 21, 1999 this sequence version replaced g1:4375971.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known: 800 n's separate
segments. Unfinished: d3469D22 Contig_ID: 01101 acc=AL031284
Length: 61683 bp Unfinished: d3469D22 Contig_ID: 01792
acc=AL031284 Length: 22802 bp
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES
source
1..85285
Location/Qualifiers
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ORIGIN
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Best Local Similarity 86.3%; Pred. No. 1.48e-147;
Matches 259; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Db 2921 TTGGCCGGGACAGTGTGCTTAATGCTTAATCCAGACATTTGGAGAGCGCAAGTGGCG 2980

QY 2143 ttggccaggcgagtggtgctacacactgttaacacacacttgaggccaaagtgtggtg 2202

Db 2981 GATCACTGAGGTGAGAGTTCGAGACGACGATGACCAACATGAGAGAAACCTGTCTTA 3040

QY 2203 gatcatcgaagccgggaggttcaagaccagcctgacacagctggaagaacccactctta 2262

Db 3041 CTAATAATATCAAAATTACCGCGGCTGTGTGTCATGCTTAATCCAGTACTACAGA 3100

QY 2263 ctnaaatatcaaaattagccggcggtggtgagcagatggtctgaancttcgctactcaga 2322

Db 3101 GCGTGAAGCAGAGAAATACATCAACCCAGAGGCGGAGTGTGCTTGAAGCATAGC 3160

QY 2322 ggcagagcagaanaatttcttgaaacttgaggagcagaggttcggtgagccagancgc 2382

Db 3161 GCGATTGCACTTCAGCTGGGCAACAGAGCAAAACTCGTCTTAAAAAAGAA 3220

QY 2383 gccattgcacttcagcctggtggttaacagagcaaacctctgtccaaaaa 2442

RESULT 13
LOCUS AC005087 105984 bp DNA HTG 12-JUN-1998
DEFINITION Homo sapiens clone RG306D19, WORKING DRAFT SEQUENCE, 17 unordered
pieces.
ACCESSION AC005087
NID 93212804
VERSION AC005087.1 GI:3212904
KEYWORDS HTG; HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 105984)
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
2 (bases 1 to 105984)
Waterston, R.H.
Direct Submission
Submitted (12-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1848: contig of 1848 bp in length
* 1849: gap of unknown length
* 1866: contig of 3138 bp in length
* 5004: gap of unknown length
* 5021: contig of 2285 bp in length
* 7306: gap of unknown length
* 7322: gap of unknown length
* 10299: contig of 2977 bp in length
* 10310: gap of unknown length
* 10317: contig of 2573 bp in length
* 12889: contig of 12906 bp in length
* 12907: gap of unknown length
* 12967: contig of 2744 bp in length
* 15651: gap of unknown length
* 15668: contig of 3842 bp in length
* 19510: gap of unknown length
* 19527: contig of 3429 bp in length
* 22955: gap of unknown length
* 22972: contig of 3402 bp in length
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Note: remainder of annotations omitted

Query Match	Score	DB	Length
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Best Local Similarity 84.9%; Pred. No. 1.48e-147;

Matches	265;	Conservative	0;	Mismatches	4/;	Indels	0;	Gaps	0;
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[illegible]

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[illegible]

b 99222 GCCCAGGCGGTGATCACCCTGAGGTTGCCAGTTCGAGACCAGCCTGACCAACATGGAG 99281

[illegible]

2189 ggccaagtgtgatcatctlaagcggtgtcaagaaccagcctgaaccaacgttgag 2248

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9928Z AALCCCLCICIAIAAAAHIAUAAAHIAUCCUCCAHUUIUUAUIC 33341

2249 aaaccatcttactnaaaatacnaaattaqccqgcgtqtaqcgcattgctgttaanc 2308

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99342 CCAGTACTCAGGAGGCTGAGGCAGGAGAATCGCTTGACC CGGAGGCAGAGGTTGCAG 99401

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2369 tgaqcccaanccqccattgcactccagcctggtaacaagacaactctgtccaaa 2428

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2429 aaaaaaaaaa 2440

RESULT 15

Accession	Length	Unit	Date
HS230G1	125515 bp	DNA	PRI 05-AUG-1998

DEFINITION Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3.

Contains EST, STS and GSS, complete sequence.

ACCESSION 284466

NID
g3319673
7844661
CT: 3310673

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KEYWORDS      HTG: Y011 3
VERSION       284466.1  GI:33196/3

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KEYWORDS: HIG; April 3.

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 125515)
 AUTHORS Wray, P.
 TITLE Direct Submission
 JOURNAL Submitted (08-JUL-1998) Chromosome X Project Group
 (http://www.sanger.ac.uk/HGP/ChrX/) Sanger Centre, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humanxys@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
 On Jul 15, 1998 this sequence version replaced gi:2578073.
 IMPORTANT: This sequence is the entire insert of clone 230G1.
 During sequence assembly data are compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variations annotated may not be found in the sequence submission
 corresponding to the overlapping clone as we submit sequences with
 only a small overlap as described above.
 This sequence was generated from part of bacterial clone contigs of
 human chromosome X, constructed by the Sanger Centre chromosome X
 mapping group. Further information can be found at
 http://www.sanger.ac.uk/HGP/ChrX/
 This sequence has been finished according to sequence map criteria
 as follows. An attempt is made to resolve all sequencing problems,
 such as compressions and repeats, but not necessarily within known
 annotated human repeat sequence elements (e.g. Alu). Where the
 sequence is ambiguous, there is an annotation using the 'unsure'
 feature key.
 The true left end of clone 230G1 is at 1 in this sequence. The true
 right end of clone 230G1 is at 125515.
 230G1 is from the library RPCI1 constructed at the Roswell Park
 Cancer Institute by the group of Pieter de Jong.
 For further details see http://dnapac.med.buffalo.edu/
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 525..778
 /note="AluIO repeat: matches 47. .300 of consensus;
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 1317..1596
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 9423..9725
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 9726..10024
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 A114161 H20205; match: H12802 AA806420 D55951 F10957
 R22909; match: AA477696 H59758 AA904128 AA32774 T85326;
 match: AA687697 H48153 H20397 R83683 AA454735; match:
 AA182638 AA222007 H44069 H21221 AA321798; match: H46375
 H19843 A573937 AA868327 AA865422; match: AA570700 H44150
 H20192 T88882 AA015618; match: H20383 T15653 H49938 H59757"

Search completed: Tue Jan 18 14:34:00 2000
Job time : 4528 secs.

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repeat_region
32725..32762
/Note="19 copies of 2 mer 97 % conserved"
prim_transcript
<32821..32877
/Note="match: multiple ESTs; match: AA282955 AA139749
AA571767 AA464040 AA824013; match: 221451 AA895634 H34312
F23024 W46769 H34604; match: AA719679 W39769 AA592343
AA92506 W54246; match: AA173069 AA425177 AA073466 W85747
AA768214; match: AA529912 AA680646 AA569136 AA896025
AA795810; match: AA152133 N6316 H40687 C81397 D57292;
match: AA800504 AA273500 N34338 AA416411 AA468169; match:
AA177766 AA634885 AA807739 C86673 N49127; match: AA175033
HSU46225 AA798480 AA272163 M79073; match: AA219027
AA105708 AA412536 C81242 AA003677; match: AA475009
AA882016 H86687 C81219 H33662; match: Z98492 AA233775
T08746 AA433377 AA619526; match: R69671 AA435188 AA760097
H99588 AA763904"
prim_transcript
<32961..329746
/Note="match: multiple ESTs; match: H16234 H59757 AA182732
AA477696 R23011; match: T85154 AA573937 R83682 AA54787
AA236603; match: H45737 T77405 F13363 N76413 W85093"
repeat_region
35727..35875
/Note="MIR repeat: matches 8..167 of consensus"
prim_transcript
<37193..372756
/Note="match: multiple ESTs; match: R16511 T19961 R41881
N48906 T19860; match: AA458501 H05270 AA442994; match:
AA144162 AA119507 AA851630 AA114188 AA866788; match:
AA104043 W88083 AA231365 AA637261 W98335; match: AA434797
AA518513 AA119507 AA800636 AA866788; match: R17266 R96026
AA346254 AA134624 R71984"
repeat_region
37462..37572
/Note="MIR repeat: matches 146..34 of consensus"
repeat_region
38310..38485
/Note="MIR repeat: matches 260..84 of consensus"
repeat_region
39291..39412
/Note="MIR repeat: matches 188..68 of consensus"
repeat_region
39826..40528
/Note="MER4C repeat: matches 728..4 of consensus"
repeat_region
41470..41739
/Note="AluSq repeat: matches 303..35 of consensus;
incomplete repeat"
prim_transcript
43206..43642
/Note="match: 3' EST AA033820 clone 375753"
repeat_region
44018..44331
Note: remainder of annotations omitted.

Query Match 9.2%; Score 223; DB 29; Length 125515;
Best Local Similarity 86.3%; Pred. No. 9.48e-147;
Matches 258; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Db 70117 TGGCCAGGCGTGGTCATGCTGTAACTTGTGAGGCCAAACGGGTGG 70176
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 2144 tggccagcgcgagtcgctacacgttaatcccaacattgggagcgcaagtggtg 2203

Db 70177 ATCAGCTGAGTGGGAGTTCAAGACCACTGGCCACAATGTGAACCCATCTAC 70236
||||| ||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 2204 atcatctaagcgcgaggtcaagcaccgctgagcaacgctgagagaaacccatctac 2263

Db 70237 TAAATAATACAAATTAGCCAGGTGTGTGGCAATGCTGTATCCAGCTACTTGGGAG 70296
||||| ||||||| ||||||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2264 tnaaaatacnaaatagccggcgctgtgtagcgatgctgtanacctggtactcagagag 2323

Db 70297 GCTGAGGCAAGAGATGCTTGAACCTGGAGGCGGAGGTGACGTGAGCCAAAGATCGCG 70356
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2324 gccgagcgcaanaatttctgaactgagcgagcgaggtgctgagccagancgcy 2383

Db 70357 CCATTGCACTCCAGCTGGGCAACAGAACAACTCCCTCAAAAAAAAAAAAAA 70415
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 2384 ccattgactccagcctggttaacagcaaacactgtccaaaaaaaaaaaaa 2442
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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated.

Sequence:

PAM	150
Gap	11

Post-processing: Minimum Match 0%

Database: sptrembl9

13:sp_vertebrate 14:sp_virus

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result	Query
No.	Score Match Length DB ID Description Pred. No.

1	225	17.1	279	11	Q62117	FAS LIGAND.	1.59E-22
2	216	16.4	240	4	Q75476	LIGAND FOR HERPESVIRUS	1.06E-22
3	208	15.8	240	4	Q43557	TUMOR NECROSIS FACTOR	4.26E-22
4	203	15.4	233	6	Q77764	TUMOR NECROSIS FACTOR	4.12E-22
5	200	15.2	234	6	Q28320	TUMOR NECROSIS FACTOR	1.65E-15
6	184	14.8	157	4	Q63820	TNF-ALPHA.	1.56E-15
7	189	14.4	232	11	Q35857	TUMOR NECROSIS FACTOR	2.52E-11
8	179	13.6	223	11	Q35734	TUMOR NECROSIS FACTOR	2.39E-11
9	177	13.5	156	11	Q63236	TUMOR NECROSIS FACTOR	2.04E-11
10	175	13.3	233	6	Q18779	TUMOR NECROSIS FACTOR.	4.93E-11
11	157	11.9	317	4	Q14788	TUMOR NECROSIS FACTOR	1.19E-11
12	154	11.7	245	4	Q14783	RANKL.	2.78E-11
13	152	11.6	216	11	Q70332	TRANCE (FRAGMENT).	9.83E-11
14	130	9.9	316	11	Q35306	TUMOR NECROSIS FACTOR.	2.27E-11
15	130	9.9	316	11	Q35335	TNF-RELATED ACTIVATION	1.71E-06
16	104	7.9	659	5	Q27878	TNF-RELATED ACTIVATION	1.71E-06
17	101	7.7	104	6	Q27878	T26G12.3 PROTEIN.	2.70E-07
18	101	7.7	800	5	Q21145	TNFA (FRAGMENT).	7.61E-07
19	100	7.6	465	2	Q21145	KOZELL.1 PROTEIN.	7.61E-07
20	100	7.6	761	13	P70009	CA. THERMOCILLUM BETA-G NA+H+ ANTIPOLYMER.	1.07E-01

ALIGNMENTS

RESULT	1		
ID	061217	PRELIMINARY;	PRT; 279 AA.
AC	061217;		
DT	01-NOV-1996 (TREMBLREL. 01 CREATED)		
DT	01-NOV-1996 (TREMBLREL. 01 LAST SEQUENCE UPDATE)		
DT	01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)		
DE	FAS LIGAND.		
OS	MUS MUSCULUS (MOUSE).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;		
OC	SCIUROGNATHI; MURIDAE; MURINAE; MUS.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-BALB/C;		
RA	FENNER M.H., SHIODA T., ISSELEBACHER K.J.;		
DR	SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.		
DR	EMBL: U58995; G1389772; -		
DR	PROSITE: PS00251; TNF_1, 1.		
DR	PFAM: PF00229; TNF; 1.		
QO	SEQUENCE 279 AA; 31340 MW; 9062DF08 CRC32;		

Query Match	17.1%;	Score 225;	DB 11;	Length 279;
Best Local Similarity	34.6%;	Pred. No. 1.59e-24;		
Matches	53;	Conservative	32;	Mismatches 51;
			Indels 17;	Gaps 13

DT	01-NOV-1998	(TREMBLEREL. 08, CREATED)
DT	01-NOV-1998	(TREMBLEREL. 08, LAST SEQUENCE UPDATE)
DT	01-NOV-1998	(TREMBLEREL. 08, LAST ANNOTATION UPDATE)
DE	LIGAND FOR HERPESVIRUS ENTRY MEDIATOR.	
Db	143	SVATHLGNHSSS-IP-LEWEDDTGFLDLSG-VKRRKGLVINEAGLYPVYSKYFRGO-198
Qy	23	PVVRQPTPHFKNQNPALHMEHGLAFETKRNRRYINIKFLIPESDSDRITYISQVFRMT-82
Db	199	S-CNN--Q--P-LNH-KVYR-R-NSKRYODLVMEERKRLNTCTTGQIMASSITLAVF-24
Qy	83	SESEELRRQGRNKKDSTIVYITKVDSTYPPQLLMGTR-SYCEVGSNWFOPIYLGAMF-141
Db	248	NLTSADHLVYNISQLINP-EESKTEFGLYKL-279
Qy	142	SLOEGDKLMVNVSDISLVDYTKREDTFFGFAFL-174
RESULT	2	
AC	075476	PRELIMINARY; PRT; 240 AA.
DT	01-NOV-1998	(TREMBLEREL. 08, CREATED)
DT	01-NOV-1998	(TREMBLEREL. 08, LAST SEQUENCE UPDATE)
DT	01-NOV-1998	(TREMBLEREL. 08, LAST ANNOTATION UPDATE)
DE	LIGAND FOR HERPESVIRUS ENTRY MEDIATOR.	

GN HYEM-L.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES.
OC CARNIVORINII; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RA HARROP J.A., McDONNELL P.C., BRIGHAM-BURKE M., IYN S.D., MINTON J.,
RA TAN K.B., DEDE K., SPAMPANATO J., SILVERMAN C., HENSLEY P.,
RA DIPRINZIO R., EMERY J.G., DEEN K., EICHMAN C., CHABOT-FLETCHER M.,
RA TRUNCH A., YOUNG P.R.;
RT HYEM-L., a novel ligand for HYEM/TR2, stimulates NF-kB-dependent
RT transcription, proliferation of T cells and inhibition of HT29 cell
RT growth.";
RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RA SHINTANI Y., NISHI K., LYNN S.D., YOUNG P.R.;
RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF064090; G3283356; -;
SQ SEQUENCE 240 AA; 26350 MW; 3490EB77 CRC32;

Query Match	16.48;	Score 216;	DB 4;	Length 240;
Best Local Similarity	32.98;	Pred. No. 1.06e-22;		
Matches	46;	Conservative	38;	Mismatches 42;
			Indels 14;	Gaps 8

[illegible]

RESULT	3	PRELIMINARY:	PRT:	240 AA.
ID	043557			
AC	043557:			
DT	01-JUN-1998	(TREMBLREL. 06, CREATED)		
DT	01-JUN-1998	(TREMBLREL. 06, LAST SEQUENCE UPDATE)		
DT	01-JUN-1998	(TREMBLREL. 06, LAST ANNOTATION UPDATE)		
DE	TUMOR NECROSIS FACTOR SUPERFAMILY MEMBER LIGHT.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;			
OC	CATARRHINI; HOMINIDAE; HOMO.			
OC	[1]			
RP	SEQUENCE FROM N.A.			
RA	MAURI D.N., EBBER R., MONTGOMERY R.I., KOCHER K.D., CHEUNG T.C.,			
RA	YU G.-L., RUBEN S., MURPHY M., ELSENBURG R.J., COHEN G.H., SPEAR P.G.,			
RA	WARE C.F.,			
RL	IMMUNITY 8:21-30(1998).			
RL	EMBL: AF036581, G281624, -.			
DQ	SEQUENCE 240 AA; 26351 MW; 44AB603A CRC32;			

Query Match	15.8%;	Score 208;	DB 4;	Length 240;
Best Local Similarity	32.1%;	Pred. No. 4.26e-21;		
Matches	45;	Conservative	38;	Mismatches 43;
			Indels 14;	Gaps 8

[illegible]

RESULT	4	PRELIMINARY;	PRT;	233 AA.
ID	077764			
AC	077764;			
DT	01-NOV-1998 (TREMBLREL, 08, CREATED)			
DT	01-NOV-1998 (TREMBLREL, 08, LAST SEQUENCE UPDATE)			
DT	01-NOV-1998 (TREMBLREL, 08, LAST ANNOTATION UPDATE)			
DE	TUMOUR NECROSIS FACTOR ALPHA.			
GN	TNF.			
OS	MACROPUS EUGENII (TAMMAR WALLABY).			
OC	EUKARYOTA; METAFAA; CHORDATA; VERTEBRATA; MAMMALIA; METATHERIA;			
OC	DIPROTODONTIA; MACROPODIDAE; MACROPUS.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=MAMMARY-ASSOCIATED LYMPH NODE;			
RA	HARRISON G.A., BROUGHTON M.J., DEANE E.M., COOPER D.W.;			
RL	SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.			
DR	EMBL: AF055915; G3659513; -			
DR	PROSITE, PS00251; TNF.1: 1.			
EQ	SEQUENCE 233 AA; 25696 MW; 5B4CAE1E CRC32;			

Query Match	15.48;	Score 203;	DB 6;	Length 233;
Best Local Similarity	25.78;	Pred. No. 4.21e-20;		
Matches	35;	Conservative	39;	Mismatches 57;
				Indels 5;
				Gaps 4;

[illegible]

RESULT	5	PRELIMINARY;	PRT;	234 AA.
ID	Q28320			
AC	Q28320;			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)			
DE	TNF ALPHA.			
OS	CAPRA HIRCUS (GOAT).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;			
NC	ARTIODACTYLIA; RUMINANTIA; PECORA; BOVIDEA; BOVIDAE; CAPRINAE; CAPRA			
FN	[1]			
RP	SEQUENCE FROM N.A.			
RA	TAKAKURA H., MORI Y., TATSUMI M.;			
RT	"Molecular cloning of caprine TNF-alpha cDNA and its expression in			
RT	E.coli and insect cells."			
RL	SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.			
DR	EMBL: D86587; D1013817; TO EMBL/GENBANK/DBJ DATA BANKS.			
DR	PROSITE: P500251; TNF_L; 1.			
DR	PFAM: PF00229; TNF; 1.			
Q0	SEQUENCE 234 AA; 2519 MW; C6424744 CRC32;			

Query Match	15.2%;	Score 200;	DB 6;	Length 234;
Best Local Similarity	28.7%;	Pred. No. 1.66e-19;		
Matches	39;	Conservative	31;	Mismatches 61;
			Indels	5;
			Gaps	5;

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Db      103 LRMGDSYAAALKAANVELKDNQVLVPFNDGLYLISQVLEPG-RG-CPSRPPLF-LHTITSR 15
      40 LHMHEHLGLAEFKKNNNTNTNFFLIPSGDFTIYSQVTRGMSSECSLROAGRNKPKDS 99
Qy      160 IAVSYQTKVNIISAISKCHRETEGAE-AKPWPEPIYQGVFOLEKGRDRLSAELNPEY 218
      100 ITVVI-TVKTSIDYPPPTQLMGTRKSVCVEGSSNMFGPIYIGAMFSQDEGDKLWVNVSDSL 158
Db      219 LDYAESGQVYFGITALL 234
      :||: :||: |

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QY 159 VDYTKEDKTEFGALL 174

Query Match	14.88;	Score 194;	DB 4;	Length 157;
Best Local Similarity	27.98;	Pred. No. 2.52e-18;		
Matches	38;	Conservative	34;	Mismatches 59;
			Indels	5;
			Gaps	5;

RESULT	7		
ID	035853	PRELIMINARY;	PRT; 232 AA.

DT 01-JAN-1998 (TREMBLREL, 05, CREATED)
DT 01-JAN-1998 (TREMBLREL, 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL, 08, LAST ANNOTATION UPDATE)
DE TIMOR NECROSIS FACTOR ALPHA.
GN TNFA.
OS MUS MUSCULUS (MOUSE)
OC EKRAYOTR; METRIZO; CHODATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIDUOGNATHI; MURIDAE; MORINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/J;
RX MEDLINE: 97246744.
RA IRAOI F., TEALE A.;
RT "Cloning and sequencing of the tnfa genes of three inbred mouse
RT strains";
RL IMMUNOGENETICS 45:459-461(1997).
RE EMBL: U68414; G2304957; _
DR PROSITE: P500251; TNF_1; 1.
DR PRAM: PF00229; TNF; 1.
SQ SEQUENCE 232 AA; 25513 MW; 982B3B306 CRC32;

Query Match	14.48;	Score 189;	DB 11;	Length 232;
Post Total Similarity	57.48;	Score 117;	DB 30;	Length 17

Matches 37; Conservative 34; Mismatches 60; Indels 4; Gaps 4;

Db 102 LEWLSQRANALLANGMDLKDNLVVPADGLYLVYSQVLEKQ-G-CPDYVLLTHTVSRFA 155

40 LHWHEHELGLAFTKNRMNTNKFLLIPESGDYFISSQVTFRGMTSECESEIRQAGRPNKPDS 99

DB 160 1SYQ-EKVNLLSAVKSPCKPDIPEGAELKP-WYEP1YLGVEFQLEKGDQLSAEVLNPKYL 217

QY	100	ITVAVIKRVDSPEPTQLLMGKVCCEGNSMNPITLGMFSLQBGDKLMMNVSDISLV	15
QY	160	DYTKEDKTFEGAFLL	174

RESULT	8	
ID	035734	PRELIMINARY;
AC	035734	PRT; 233 AA

DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE TUMOR NECROSIS FACTOR ALPHA PRECURSOR.
 GN TNF-ALPHA OR TNF ALPHA.
 OS MARMOTA MONAX (WOODCHUCK).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA
 OC SCIUROGNATHI; SCIURIDAE; SCIURINAE; MARMOTA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PBMC.
 RX MEDLINE; 98139533.
 RA LOHRENGEL B., LU M., ROGGENDORF M.;
 RT "Molecular cloning of the woodchuck cytokines: TNF-alpha, IFN-gamma,
 RI and IL-6."
 RL IMMUNOGENETICS 47:332-335(1998).

RP	SEQUENCE FROM N.A.			
RC	TISSUE-PERIPHERAL BLOOD:			
RA	ZHOU H., HU J., SEEGER C.;			
RL	SUBMITTED (AUG-1998) TO EMBL/GENBANK/DDBJ DATA BANKS			
DR	EMBL; Y14133; E348344; -			
DR	EMBL; AF082491; G3450964; -			
DR	PROSITE; PS00251; TNF_1; 1.			
DR	PFAM; PFO0229; TNF; 1.			
KW	SIGNAL.			
FT	SIGNAL.	1	77	POTENTIAL.
FT	CHAIN	78	233	POTENTIAL.
SQ	SEQUENCE	233 AA;	25764 MW;	6FC0F34A CRC32;

Query Match	13.68;	Score 179;	DB 11;	Length 233;
Best Local Similarity	29.9%;	Pred. No. 2.04e-15;		
Matches	41; Conservative	33; Mismatches	55; Indels	8; Gaps 5

Db 103 LVWLSRRANALLANGMELIDNQLVVPANGLYLVYSQVLEFKGQGCPSVLLTHTVSRFAVS 162

QY 40 LHWEHELGLAFTKNRMNYTNKFLIPESGDYFIYSQVTFRGMT-SECSEIRQA-GRPNKP 97

Db 163 YQDKVNLLSAIKS-PCPKESLEGA---EFKP-WYEPIYLGVFELQKGDRLSAEVLPS 216

QY 98 DSITVITKVTDSYPEPTÖLLMGTKSVCEVGSNWEPPIYLGAMFSLÖEGDKLMVNSDIS 157

Db 217 YLDEAESCQVFEVIAL 233

RESULT	9
ID	Q62326
	PRELIMINARY; PRT; 156 AA

DT	01-NOV-1996	(TREMELREL, 01, CREATED)
DT	01-NOV-1996	(TREMELREL, 01, LAST SEQUENCE UPDATE)
DT	01-NOV-1998	(TREMELREL, 08, LAST ANNOTATION UPDATE,
DE		TUMOR NECROSIS FACTOR.

OC EUKARYOTA; METAZOA; CHORATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA
OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.

RP SEQUENCE FROM N. A.
RX MEDLINE; 86149365.
RA CAUT D., BEUTLER B., HARTOG K., THAYER R., BROWN-SHIMER S.
RA CERAMI A.;


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OY 42 WEHELGLAFTKRNMTYTNKFLIPESGDIYFISQYTFEGMTSECEINQAGRPKNKPDST 101
DB 168 VYVTKTSIKIPSSHTLMKSGSTKYNMSEPHYSINVGFEFKLRSGEISIEVNSPSL 227
OY 102 VVITKVTDSYPEPTQLMGTKSVC-EVGSNM-FQPIYLGAMFSLQEGDKLMVNSDISLV 159
DB 228 D-PDODATYFGAF 239
OY 160 DYTEKEDKTEFGAF 172

RESULT 13
ID 070332 PRELIMINARY; PRT; 216 AA.
AC 070332;
DT 01-JAN-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR-ALPHA (FRAGMENT).
OS MESOCRICEUTUS AURATUS (GOLDEN HAMSTER).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCUROGNATHI; MURIDAE; CRICETINAE; MESOCRICEUTUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SPLEEN;
RA MEDLINE; 98234044.
RA MELBY P.C., TRYON V.V., CHANDRASEKAR B., FREEMAN G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT analysis of cytokine mRNA expression in experimental visceral
RT leishmaniasis".
RL INFECT. IMMUN. 66:2135-2142(1998).
DR EMBL; AF046215; G3005109; -.
DR PROSITE; PS00251; TNF_1; 1.
FT NON_TER 1
FT NON_TER 216
SQ SEQUENCE 216 AA; 23793 MW; 79A08367 CRC32;

Query Match 11.6%; Score 152; DB 11; Length 216;
Best Local Similarity 27.6%; Pred. No. 2,27e-10;
Matches 34; Conservative 31; Mismatches 54; Indels 4; Gaps 4;

DB 95 LEWLSHRANALLANGMSLKDNOVLVPADGLYVYSGVFRQO-G-CPSYVLLHTHSRIA 152
OY 40 LMEHELGLAFTKRNMTYTNKFLIPESGDIYFISQYTFEGMTSECEINQAGRPKNKPD 99
DB 153 VSYE-DVNYLLSAIKSPKPEGEELK-P-WYEPYIYGVOLEKGDRLSAEYNLPKYL 210
OY 100 ITVITKVTDSYPEPTQLMGTKSVCYGVSNMFPQIYLGAMFSLQEGDKLMVNSDISLV 159
DB 211 DPA 213
OY 160 DYT 162

RESULT 14
ID 035306 PRELIMINARY; PRT; 316 AA.
AC 035306;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TNF-RELATED ACTIVATION-INDUCED CYTOKINE (RANKL).
GN TRANCE OR RANKL.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BONE MARROW;
RA MEDLINE; 98032977.
RA ANDERSON D.M., MARASKOVSKY E., BILLINGSLEY W.L., DOUGALL W.C.,
RA TOMETSKO M.E., ROUX E.R., TEEPE M.C., DUBOSE R.F., COSMAN D.,
RA GALIBERT L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";

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RL NATURE 390:175-179(1997).
DR EMBL; AF019048; G2612924; -.
DR MGD; MGI:1100089; TRANCE.
DR PFAM; PF00229; TNF; 1.
SQ SEQUENCE 316 AA; 35002 MW; 97DA4504 CRC32;

Query Match 9.9%; Score 130; DB 11; Length 316;
Best Local Similarity 26.3%; Pred. No. 1.71e-06;
Matches 35; Conservative 33; Mismatches 55; Indels 10; Gaps 9;

DB 186 WYHDRGMA-KISMTLSNGKLRVNOGFFYLYLANICFRHETS-GSV-PTD--Y-LQ-LM 238
OY 42 WEHELGLAFTKRNMTYTNKFLIPESGDIYFISQYTFEGMTSECEINQAGRPKNKPDST 101
DB 239 VYVTKTSIKIPSSHTLMKSGSTKYNMSEPHYSINVGFEFKLRAGEISIOVNSPSL 298
OY 102 VVITKVTDSYPEPTQLMGTKSVC-EVGSNM-FQPIYLGAMFSLQEGDKLMVNSDISLV 159
DB 299 D-PDODATYFGAF 310
OY 160 DYTEKEDKTEFGAF 172

RESULT 15
ID 035235 PRELIMINARY; PRT; 316 AA.
AC 035235;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TNF-RELATED ACTIVATION-INDUCED CYTOKINE (TRANCE).
GN TRANCE.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 97460112.
RA WONG B.R., RHO J., ARRON J., ROBINSON E., ORLINICK J., CHAO M.,
RA KALACHIKOV S., CAVANI E., BARTLETT F.S. III, FRANKEL W.N., LEE S.Y.,
RA CHOI Y.;
RT "TRANCE is a novel ligand of the tumor necrosis factor receptor
RT family that activates C-Jun N-terminal kinase in T cells.";
RL J. BIOL. CHEM. 272:25190-25194(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE; 98227661.
RA LACEY D.L., TIMMS E., TAN H.-L., KELLEY M.J., DUNSTAN C.R.,
RA BURGESS T., ELLIOTT R., COLOMERO A., ELLIOTT G., SCULLY S., HSU H.,
RA SULLIVAN J., HAWKINS N., DAVY E., CAPPAPELLI C., ELI A., QIAN Y.-X.,
RA KAUFMAN S., SAROSI I., SHALHOUB V., SENALDI G., GUO J., DELANEY J.,
RA BOYLE W.J.;
RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT differentiation and activation.";
RL CELL 93:165-176(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-BONE MARROW;
RX MEDLINE; 98188248.
RA YASUDA H., SHIMA N., NAKAGAWA N., YAMAGUCHI K., KINOSAKI M.,
RA MCHIZUKI S., TOMOIYASU A., YANO K., GOTO M., MURAKAMI A., TSUDA E.,
RA MORINAGA T., HIGASHIO K., UDAGAWA N., TAKAHASHI N., SUDA T.;
RT "Osteoclast differentiation factor is a ligand for
RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
RT to TRANCE/RANKL.";
RL PROC. NATL. ACAD. SCI. U.S.A. 95:3597-3602(1998).
DR EMBL; AF053713; G3057148; -.
DR EMBL; AF013170; G2411498; -.
DR EMBL; AB008426; D1026353; -.
DR MGD; MGI:1100089; TRANCE.
DR PFAM; PF00229; TNF; 1.
SQ SEQUENCE 316 AA; 34944 MW; F76EC806 CRC32;

Query Match 9.9%; Score 130; DB 11; Length 316;

```

Best Local Similarity 26.3%; Pred. No. 1.71e-06;
Matches 35; Conservative 33; Mismatches 55; Indels 10; Gaps 9;

Db	186	WYHDSGMA-KISNMTLSNGKLRVNDGFFYLXANICFRHETS-GSV-PTD--Y-LQ-LM	238
QY	42	WEHGLAFTKRNMYTNKFLIPESGDYFTYQVTFRGMTSECSSEIRQGRPNKPDST	101
Db	239	VYVVKTSIKIPSSHNLKGGSTKNMNSGSEFHFYSINVGPFKLRAGEISIQVSNPSLL	298
QY	102	VVITKVTDSYPEPTQLMGTKSVC-EVGSNW-FQPIYLGAMFSLQEGDKLWVNSDISLV	159
Db	299	D-PDQDATYFGAF	310
QY	160	DYTKEDKTEFFGAF	172

Search completed: Tue Jan 18 13:22:22 2000
Job time : 72 secs.

 M I S E R I E (TM)

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MPsrch_LP protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Jan 18 13:20:29 2000; MasPar time 6.81 Seconds
 Tabular output not generated.

Title: >US-09-246-129-2
 Description: (1-174) from US09246129A.pep
 Perfect Score: 1314
 Sequence: 1 MKRFLSKYSPMKRLILFL.....DISLVYTKEDKTFEGAFLL 174

Scoring table: PAM 150
 Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 45.305; Variance 75.582; scale 0.599

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.	
1	242	18.4	202	1	TNFB_RAT	LYMPHOTOXIN-ALPHA PREC	4.89e-29
2	241	18.3	202	1	TNFB_MOUSE	LYMPHOTOXIN-ALPHA PREC	8.00e-29
3	235	17.9	291	1	TRAI_MOUSE	TNF-RELATED APOPTOSIS	1.52e-27
4	232	17.7	279	1	FASL_MOUSE	FAS ANTIGEN LIGAND	6.56e-27
5	231	17.6	281	1	TRAI_HUMAN	TNF-RELATED APOPTOSIS	1.07e-26
6	229	17.4	197	1	TNFB_HUMAN	LYMPHOTOXIN-ALPHA PREC	2.83e-26
7	229	17.4	204	1	TNFB_BOVIN	LYMPHOTOXIN-ALPHA PREC	2.83e-26
8	220	16.7	281	1	FASL_HUMAN	FAS ANTIGEN LIGAND (AP	2.20e-24
9	217	16.5	204	1	TNFB_PIG	LYMPHOTOXIN-ALPHA PREC	9.32e-24
10	212	16.1	278	1	FASL_RAT	FAS ANTIGEN LIGAND	1.02e-22
11	200	15.2	205	1	TNFB_HUMAN	LYMPHOTOXIN-ALPHA PREC	3.00e-20
12	200	15.2	233	1	TNFA_MACFA	TUMOR NECROSIS FACTOR	3.00e-20
13	198	15.1	233	1	TNFA_TRIUV	TUMOR NECROSIS FACTOR	7.68e-20
14	197	15.0	233	1	TNFA_MACMU	TUMOR NECROSIS FACTOR	1.23e-19
15	197	15.0	233	1	TNFA_PAPHU	TUMOR NECROSIS FACTOR	1.23e-19
16	196	14.9	193	1	TNFA_CAPHI	TUMOR NECROSIS FACTOR	1.96e-19
17	196	14.9	232	1	TNFA_PIG	TUMOR NECROSIS FACTOR	1.96e-19
18	194	14.8	233	1	TNFA_HUMAN	TUMOR NECROSIS FACTOR	1.96e-19
19	191	14.5	233	1	TNFA_PAPSP	TUMOR NECROSIS FACTOR	2.01e-18
20	191	14.5	233	1	TNFA_CANPA	TUMOR NECROSIS FACTOR	2.01e-18
21	191	14.5	306	1	TNFC_MOUSE	LYMPHOTOXIN-BETA (LT-B	2.01e-18
22	189	14.4	234	1	TNFA_SHEEP	TUMOR NECROSIS FACTOR	5.07e-18
23	189	14.4	235	1	TNFA_MOUSE	TUMOR NECROSIS FACTOR	5.07e-18

24	187	14.2	234	1	TNFA_HORSE	TUMOR NECROSIS FACTOR	1.28e-17
25	187	14.2	235	1	TNFA_PERLE	TUMOR NECROSIS FACTOR	1.28e-17
26	184	14.0	234	1	TNFA_CAVPO	TUMOR NECROSIS FACTOR	5.08e-17
27	181	13.8	235	1	TNFA_RABIT	TUMOR NECROSIS FACTOR	2.01e-16
28	176	13.4	235	1	TNFA_RAT	TUMOR NECROSIS FACTOR	1.95e-15
29	175	13.3	233	1	TNFA_BOVIN	TUMOR NECROSIS FACTOR	3.06e-15
30	171	13.0	229	1	TNFA_CEREL	TUMOR NECROSIS FACTOR	1.85e-14
31	169	12.9	233	1	TNFA_FELCA	TUMOR NECROSIS FACTOR	4.53e-14
32	138	10.5	244	1	TNFC_HUMAN	LYMPHOTOXIN-BETA (LT-B	2.87e-08
33	101	7.7	384	1	RCI2_ECOLI	SHUFFLON-SPECIFIC DNA	4.17e-02
34	101	7.7	384	1	RCI1_ECOLI	SHUFFLON-SPECIFIC DNA	4.17e-02
35	100	7.6	261	1	CD40_HUMAN	CD40 LIGAND (CD40-L) (5.89e-02
36	98	7.5	552	1	CITA_ECOLI	SENSOR KINASE CITA (EC	1.17e-01
37	97	7.4	261	1	CD40_BOVIN	CD40 LIGAND (TNF-RELAT	1.64e-01
38	96	7.3	1647	1	SN24_HUMAN	POSSIBLE GLOBAL TRASC	2.30e-01
39	95	7.2	260	1	CD40_MOUSE	CD40 LIGAND (TNF-RELAT	3.20e-01
40	93	7.1	502	1	VL2_HPV48	MINOR CAPSID PROTEIN L	6.19e-01
41	92	7.0	822	1	MAH1_CRIGR	SODIUM/HYDROGEN EXCHAN	8.57e-01
42	91	6.9	245	1	YB7_YEAST	HYPOTHETICAL 28.1 KD P	1.18e+00
43	91	6.9	521	1	MET3_YEAST	SULFATE ADENYLTRANSFER	1.18e+00
44	91	6.9	551	1	FIXN_AZOCA	CYCLOCHROME C OXIDASE P	1.18e+00
45	90	6.8	1638	1	BRW_DROME	HOMOTIC GENE REGULATO	1.63e+00

ALIGNMENTS

RESULT 1
 ID TNFB_RAT STANDARD; PRT: 202 AA.

AC 006332;

DT 01-JUN-1994 (REL. 29, CREATED)

DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE LYMPHOTOXIN-ALPHA PRECURSOR (LT-ALPHA) (TNF-BETA).

GN LTA OR TNFB.

OS RATTUS NORVEGICUS (RAT).

OC EUKARIOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC RODENTIA; SCIUROGNATHI; MORIDAE; MURINAE; RATTUS.

RP [1]

RC STRAIN-SPRAGUE-DAWLEY; TISSUE-TESTIS;

RX MEDLINE; 94040766.

RA KWON J., CHUNG I.Y., BENVENISTE E.N.;

RT "Cloning and sequence analysis of the rat tumor necrosis

factor-encoding genes.";

RL GENE 132:227-236(1993).

CC -!- FUNCTION: LYMPHOTOXIN IS A CYTOKINE PRODUCED BY LYMPHOCYTES WHICH

IS CYTOTOXIC FOR A WIDE RANGE OF TUMOR CELLS IN VITRO AND IN VIVO.

CC -!- SUBUNIT: HETEROTRIMER OF EITHER TWO BETA AND ONE ALPHA SUBUNITS

OR (LESS PREVALENT) TWO ALPHA AND ONE BETA SUBUNITS.

CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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CC -----

DR EMBL; L00981; G205255; -.

DR PIR; J00869; J00869.

DR PROSITE; PS00251; TNF_1; 1.

DR PROSITE; PS00409; TNF_2; 1.

DR PIR; PF00229; TNF; 1.

KW CYTOKINE; GLYCOPROTEIN; CYTOTOXIN; SIGNAL.

FT SIGNAL 1 33 BY SIMILARITY.

FT CHAIN 34 202 LYMPHOTOXIN-ALPHA.

FT CARBOHYD 94 94 POTENTIAL.

SEQUENCE 202 AA; 22111 MW; 66200504 CRC32;

Query Match 18.4%; Score 242; DB 1; Length 202;

Best Local Similarity 36.5%; Pred. No. 4.89e-29;

RA WILEY S.R., SCHOOLEY K., SMOLAK P.J., DIN W.S., HUANG C.-P.,
 RA NICHOL J.K., SUTHERLAND G.R., DAVIS-SMITH T., RADUCH C., SMITH C.A.,
 RA GOODWIN R.G.;
 RT "Identification and characterization of a new member of the TNF
 RT family that induces apoptosis.";
 RL IMMUNITY 3:673-682(1995).
 CC -1- FUNCTION: INDUCES APOPTOSIS.
 CC -1- SUBUNIT: HOMOTRIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: WIDESPREAD.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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 CC -----
 DR EMBL: U37522; G1149560; -.
 DR MGD: MGI:107414; TRAIL.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 DR PIRAM: P00229; TNF; 1.
 DR CYTOKINE: TRANSMEMBRANE; SIGNAL-ANCHOR: APOPTOSIS.
 KW DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DOMAIN 39 291 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 52 52 POTENTIAL.
 SQ SEQUENCE 291 AA: 33477 MW: F9906FBE CRC32;
 Query Match 17.9%; Score 235; DB 1; Length 291;
 Best Local Similarity 31.4%; Pred. No. 1,52e-27;
 Matches 43; Conservative 35; Mismatches 51; Indels 8; Gaps 8;
 Db 158 WESSRKGHSL-NHVLFRNCELYIEQGLYIYSQYFFQEAR-DASWMSKDYKIKQ 215
 QY 42 WEHEL-GLAFTKRNMYTNKFLIPESGYFIYSQYTFPGMTSECEIRQAGRPN-KPDS 99
 Db 216 LVQYIKYKT-SYDPPIVLMKSARNSQMSRDAEYGLSYISQGGFELKKNDRIFVSTNH 274
 QY 100 ITVITIKYVDSTPEPTOLMGTSVC-EVGSNM-FQPIYLGAFSLQESDKLMVNSDIS 157
 Db 275 LMDLDQEA-SFGGAPLI 290
 QY 158 LVDTYKEDKTFEGAPLL 174
 RESULT 4
 ID FASL_MOUSE STANDARD; PRT; 279 AA.
 AC P41047;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE FAS ANTIGEN LIGAND.
 GN APTILGI OR FASL OR GLD.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA.
 OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94185175.
 RA TAKAHASHI T., TANAKA M., BRANNAN C.I., JENKINS N.A., COPELAND N.G.,
 RA SUDA T., NAGATA S.;
 RT "Generalized lymphoproliferative disease in mice, caused by a point
 RT mutation in the fas ligand";
 RL CELL 76:969-976(1994).
 RN [2]
 RP SEQUENCE FROM N.A., AND 3D-STRUCTURE MODELLING.
 RC STRAIN=C57BL/6;
 RX MEDLINE: 95388076
 RA PEITSCH M.J., TSCHOPP J.J.;

RT "Comparative molecular modelling of the Fas-ligand and other members
 RT of the TNF family";
 RL MOL. IMMUNOL. 32:761-772(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95196085.
 RA LYNCH D.H., WATSON M.L., ALDERSON M.R., BAUM P.R., MILLER R.E.,
 RA TOUGH T., GIBSON M., DAVIS-SMITH T., SMITH C.A., HUNTER K.;
 RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
 RT TNF family gene cluster";
 RL IMMUNITY 1:131-136(1994).
 RN [4]
 RP CHARACTERIZATION OF VARIANT GLD.
 RX MEDLINE: 96091792.
 RA HANE M., PEITSCH M.C., IMLER M., SCHROETER M., LOWIN B.,
 RA ROUSSEAU M., BRON C., RENNO T., FRENCH L., TSCHOPP J.;
 RT "Characterization of the non-functional Fas ligand of gld mice";
 RL IMMUNOL. 7:1381-1386(1995).
 CC -1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
 CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
 CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
 CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
 CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
 CC T CELLS, OR BOTH.
 CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
 CC INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
 CC SURFACE.
 CC -1- DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED
 CC LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE
 CC RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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 CC -----
 DR EMBL: U06948; G473565; -.
 DR EMBL: U10984; G511222; -.
 DR EMBL: S76752; G913760; -.
 DR MGD: MGI:99255; FASL.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 DR PIRAM: P00229; TNF; 1.
 DR HSSP: P01375; 27UN.
 DR CYTOKINE: TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR: APOPTOSIS;
 KW DISEASE MUTATION.
 FT DOMAIN 1 78
 FT TRANSMEM 79 100 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 101 279 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DOMAIN 4 69 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 45 51 PRO-RICH.
 FT DISULFID 200 231 POLY-PRO.
 FT VARIANT 273 273 BY SIMILARITY.
 FT CARBOHYD 117 117 F->L (IN GLD; ABOLISH BINDING OF FASL TO
 FT CARBOHYD 182 182 ITS RECEPTOR).
 FT CARBOHYD 248 248 POTENTIAL.
 FT CARBOHYD 258 258 POTENTIAL.
 SQ SEQUENCE 279 AA: AFD64DAB CRC32;
 Query Match 17.7%; Score 232; DB 1; Length 279;
 Best Local Similarity 35.3%; Pred. No. 6,56e-27;
 Matches 54; Conservative 32; Mismatches 50; Indels 17; Gaps 13;
 Db 143 SVALTGNPHRS-IP-LEMDTYGTALISG-VKYYKGLVINEGTGYFYSAVYRGQ- 198
 QY 23 PVVROTPTQHFKNQFPALHWEHIEGLAFTKRNMYTNKFLIPESGYFIYSQYTFRGMT 82


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Db 182 HL-LTSPSSVFEGAFAL 197
   158 LVDYTKEDKTEFGAFLL 174

RESULT 7
ID TNER_BOVIN STANDARD: PRT: 204 AA.
AC 006600.
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE LYMPHOTOXIN-ALPHA PRECURSOR (LT-ALPHA) (TNF-BETA).
GN LTA OR TNFB.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLIA; RUMINANTIA; PECORA; BOVIDEA; BOVIDAE; BOVINAE; BOS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94083525.
RA CLUDTS I., CLEUTER Y., KETTMANN R., BURNY A., DROOGMANS L.;
RT "Cloning and characterization of the tandemly arranged bovine
RT lymphotoxin and tumour necrosis factor-alpha genes.";
RL CYTOKINE 5:336-341(1993).
CC -1- FUNCTION: LYMPHOTOXIN IS A CYTOKINE PRODUCED BY LYMPHOCYTES WHICH
CC IS CYTOTOXIC FOR A WIDE RANGE OF TUMOR CELLS IN VITRO AND IN VIVO.
CC -1- SUBUNIT: HETEROTRIMER OF EITHER TWO BETA AND ONE ALPHA SUBUNITS
CC OR (LESS PREVALENT) TWO ALPHA AND ONE BETA SUBUNITS.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
DR EMBL: 214137; G797.
DR PIR: S24641; S24641.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR PFAM: PF00229; TNF; 1.
DR CYTOKINE; GLYCOPROTEIN; CYTOTOXIN; SIGNAL.
FT SIGNAL. 1 33 BY SIMILARITY.
FT CHAIN 34 204 LYMPHOTOXIN-ALPHA.
FT CARBOHYD 95 95 POTENTIAL.
FT SEQUENCE 204 AA; 22098 MW; E0B38524 CRC32;

Query Match 17.4%; Score 229; DB 1; Length 204;
Best Local Similarity 35.0%; Pred. No. 2,83e-26;
Matches 48; Conservative 23; Mismatches 58; Indels 8; Gaps 8;

Db 75 STRRANDBRALRKGFSISNNLSLVPTSGLYTVSYQVVFSGR-G-GFP-R-AT-PT-PL 128
   39 ALHWHEHGLAFTKRNMTNKFLLIPESGDYFYISQVTFRGMSECEIRQAGRPKPD 98
Db 129 VLAHEVOLFSPQYPPHVPFLLSAOKSVCCGPGQPMWRYVYOGAVFLTTGGDLSSTHDSIS 188
   99 SITVITKTYDSTYPTQLMGTKSVCEVG-SNMFQPIYLGMMSLQGDGLMNVSDIS 157
Db 189 HL-LTSPSSVFEGAFAL 204
   158 LVDYTKEDKTEFGAFLL 174

RESULT 8
ID FAST_HUMAN STANDARD: PRT: 281 AA.
AC P48023.
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

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DE FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).
GN APTLIG1 OR FASL.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95105731.
RA ALDERSON M.;
RT "Fas ligand mediates activation-induced cell death in human T
RT lymphocytes.";
RL J. EXP. MED. 181:71-77(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95127560.
RA TAKAHASHI T., TANAKA M., INAZAWA J., ABE T., SUDA T., NAGATA S.;
RT "Human Fas ligand: gene structure, chromosomal location and species
RT specificity.";
RL INT. IMMUNOL. 6:1567-1574(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA SCHAEFFELIN C.E., POEHLMANN R., PHILIPPSEN P., EIBEL H.;
RL SUBMITTED (JUN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95071350.
RA MITA E., HAYASHI N., IIO S., TAKEHARA T., HIJIOKA T., KASAHARA A.,
RA FUSAMOTO H., KAMADA T.;
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus
RT infection.";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 204:468-474(1994).
RN [5]
RP SEQUENCE FROM N.A.
RA WILKINSON J.;
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
CC FAS-ANTIGEN T CELL MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
CC T CELLS, OR BOTH.
CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
CC INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
CC SURFACE.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X89102; G887456; -
DR EMBL: U08137; G624628; -
DR EMBL: U11821; G595431; -
DR EMBL: D38122; G1369902; -
DR EMBL: Z96050; E320286; -
DR MIM: 134638; -
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR PFAM: PF00229; TNF; 1.
DR HSSP: P01375; 2TUN.
KM CYTOKINE; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR; APOPTOSIS;
KM DISEASE MUTATION.
FT DOMAIN 1 80 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 81 102 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 103 281 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 4 70 PRO-RICH.
FT DOMAIN 45 65 POLY-PRO.
FT DISULFID 202 233 BY SIMILARITY.

```


QY 99 STTVVITKVDYSPEPTOLMGTKSV-C-EVGSNMFQPIYLGMFSLQEGDKLWNVSDIS 157
 DB 190 HLVL-S-PTVFGAFAL 205
 QY 158 LVDYTKEDKTEFGAFLL 174

RESULT 12
 ID TNFA_TNFA STANDARD: PRT: 233 AA.
 AC P79337;
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
 GN TNFA.
 OS MACACA FASCICULARIS (CRAB EATING MACROVE) (CYNOMOLGUS MONKEY).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; CERCOPITHECIDAE; CERCOPITHECINAE; MACACA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-LYMPHOCYTES;
 RA TATSUMI M.;
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
 WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
 CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
 CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
 OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
 CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
 CONDITIONS. (BY SIMILARITY).
 CC -1- SUBUNIT: HOMOTRIMER.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 EXTRACELLULAR SOLUBLE FORM.
 CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
 PROTEOLYTIC PROCESSING.
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
 CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
 AND MALNUTRITION.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AB000513; G1794149; -
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS0049; TNF_2; 1.
 DR PFAM: PF00229; TNF; 1.
 DR HSSP: P01375; TNF.
 KM CYTOKINE; CYTOTOXIN; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
 FT PROPEP 1 76 BY SIMILARITY.
 FT CHAIN 77 233 TUMOR NECROSIS FACTOR.
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DISULFID 145 177 BY SIMILARITY.
 SQ SEQUENCE 233 AA; 25558 MW; 856FC354 CRC32;

Query Match 15.2%; Score 200; DB 1; Length 233;
 Best Local Similarity 28.7%; Pred. No. 3,00e-20;
 Matches 39; Conservative 34; Mismatches 58; Indels 5; Gaps 5;

DB 102 LQMLNRAALVANGVELDNOVLVPSBSLYLYSOVLFEKG-G-CPS-NHYVLHTISR 158
 QY 40 LHMHEHLGLAFTKRNRYNFKLLIPESGDYFIYSQVFRGMTSCSSEIRQGRNKPDS 99
 DB 159 IAVSYOTKNTLLSAIKSPQORETPEGAE-AKPMYEPILGVFOLEKDRLSAEINLPDY 217
 QY 100 ITVVI-TKVTDSYPEPTQLMGTKSVCEVGSNMFQPIYLGMFSLQEGDKLWNVSDISL 158
 DB 218 LDFAEFGQLYFGAIAL 233

QY 159 VDYTKEDKTEFGAFLL 174

RESULT 13
 ID TNFA_TRIVU STANDARD: PRT: 233 AA.
 AC P79374;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
 GN TNFA.
 OS TRICHOSURUS VULPECULA (BRUSH-TAILED POSSUM).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; METATHERIA;
 OC DIPROTODONTIA; PHALANGERIDAE; TRICHOSURUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 96315690.
 RA WEDLOCK D.N., ALDWELL F.E., BUDDLE B.M.;
 RT "Molecular cloning and characterization of tumor necrosis factor
 alpha (TNF-alpha) from the Australian common brushtail possum,
 Trichosurus vulpecula."
 RT Trichosurus vulpecula.
 RL IMMUNOL. CELL. BIOL. 74:151-158(1996).
 CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
 WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
 CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
 CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
 OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
 CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
 CONDITIONS (BY SIMILARITY).
 CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
 CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
 PROTEOLYTIC PROCESSING (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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 CC -----
 DR EMBL: S83283; G1881812; -
 DR EMBL: AF016102; G2425046; -
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS0049; TNF_2; 1.
 DR PFAM: PF00229; TNF; 1.
 DR HSSP: P01375; TNF.
 KM CYTOKINE; CYTOTOXIN; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
 FT PROPEP 1 77 BY SIMILARITY.
 FT CHAIN 78 233 TUMOR NECROSIS FACTOR.
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DISULFID 145 177 BY SIMILARITY.
 SQ SEQUENCE 233 AA; 25704 MW; 873F8626 CRC32;

Query Match 15.1%; Score 198; DB 1; Length 233;
 Best Local Similarity 27.9%; Pred. No. 7,68e-20;
 Matches 38; Conservative 40; Mismatches 53; Indels 5; Gaps 4;

DB 102 LHWGVANTLLNGMELVDNOLVPSSTLYLYVLSQLYKG--SOGKRESLY-LTHKISR 158
 QY 40 LHMHEHLGLAFTKRNRYNFKLLIPESGDYFIYSQVFRGMTSCSSEIRQGRNKPDS 99
 DB 159 FTLSYQKVTLLANIRSSCKRAEDDGE-PSAMYEPIYLAGVFOLEKDRVDTNYPEN 217
 QY 100 ITVVI-TKVTDSYPEPTQLMGTKSVCEVGSNMFQPIYLGMFSLQEGDKLWNVSDISL 158
 DB 218 LDFAEFGQLYFGAIAL 233
 QY 159 VDYTKEDKTEFGAFLL 174

```
RESULT 14
ID TNFA_MACMU STANDARD: PRT: 233 AA.
AC P48094:
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNFA.
OS MACACA MULATTA (RHEUS MACAQUE).
OC EURKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
OC PRIMATES: CATARRHINI: CERCOPITHECIDAE: CERCOPITHECINAE: MACACA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96003435.
RA VILLINGER F.J., BRAR S.S., MAYNE A.E., CHIKKALA N., ANSARI A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates."
RL J. IMMUNOL. 155:3946-3954(1995).
CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC
DR EMBL: U19850; G644818; -
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR PIRAM: P00229; TNF; 1.
DR HSSP: P01375; TNF; 1.
KW CYTOKINE; CYTOTOXIN; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
FT PROPEP 1 76
FT CHAIN 77 233 BY SIMILARITY.
FT TRANSMEM 36 56 TUMOR NECROSIS FACTOR.
FT DISULFID 145 177 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
SQ SEQUENCE 233 AA; 25630 MW; 146A1B48 CRC32;

Query Match 15.0%; Score 197; DB 1; Length 233;
Best Local Similarity 28.7%; Pred. No. 1,23e-19;
Matches 39; Conservative 34; Mismatches 58; Indels 5; Gaps 5;
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RESULT 15
ID TNFA_PAPHU STANDARD: PRT: 233 AA.
AC 077510;
DT 15-DEC-1998 (REL. 37, CREATED)
DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNFA.
OS PAPIO HAMADRYAS URSINUS (CHACMA BABOON).
OC EURKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:
OC PRIMATES: CATARRHINI: CERCOPITHECIDAE: CERCOPITHECINAE: PAPIO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98147379.
RA HAUSER S.B., REDL H., SCHLAG G., GIROIR B.P.;
RT "Complementary DNA (cDNA) sequence of baboon tumor necrosis factor
RT alpha."
RL MOL. IMMUNOL. 34:1041-1042(1997).
CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC
DR EMBL: AF019963; G3417555; -
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR CYTOKINE; CYTOTOXIN; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
KW PROPEP 1 76
FT CHAIN 77 233 BY SIMILARITY.
FT TRANSMEM 36 56 TUMOR NECROSIS FACTOR.
FT DISULFID 145 177 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
SQ SEQUENCE 233 AA; 25658 MW; E38CF6E8 CRC32;

Query Match 15.0%; Score 197; DB 1; Length 233;
Best Local Similarity 28.7%; Pred. No. 1,23e-19;
Matches 39; Conservative 34; Mismatches 58; Indels 5; Gaps 5;
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Search completed: Tue Jan 18 13:20:53 2000
Job time : 24 secs.

 W I D E S E E R (TM)

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Msrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Jan 18 13:19:47 2000; Maspar time 9.89 Seconds
 Tabular output not generated. 704.691 Million cell updates/sec

Title: >US-09-246-129-2
 Description: (1-174) from US09246129A.pep
 Perfect Score: 1314
 Sequence: 1 MRRFLSKVYSFPMKILFL.....DISLVDYTKEDKTFGAFLL 174

Scoring table: PAM 150
 Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: pir60
 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 44.271; Variance 85.869; scale 0.516

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	242	18.4	202	2	JN0869	tumor necrosis factor	8.30e-25
2	241	18.3	202	2	B27303	tumor necrosis factor	1.27e-24
3	232	17.7	279	2	A53062	Fas ligand - mouse	5.78e-23
4	229	17.4	197	2	JH0309	tumor necrosis factor	2.05e-22
5	229	17.4	204	2	S24641	lymphotoxin - bovine	2.05e-22
6	220	16.7	281	2	I38707	Fas ligand - human	8.93e-21
7	217	16.5	204	2	S17289	tumor necrosis factor	3.12e-20
8	212	16.1	278	2	A49266	fasc ligand - rat	2.48e-19
9	200	15.2	205	1	OWHUX	lymphotoxin alpha pre	3.43e-17
10	196	14.9	193	2	S06192	tumor necrosis factor	1.75e-16
11	196	14.9	232	2	S12606	tumor necrosis factor	1.75e-16
12	194	14.8	233	1	OWHUN	tumor necrosis factor	3.93e-16
13	191	14.5	233	1	S22052	tumor necrosis factor	1.32e-15
14	191	14.5	306	2	I49139	lymphotoxin-beta - mo	1.32e-15
15	189	14.4	233	2	S13114	tumor necrosis factor	2.94e-15
16	189	14.4	234	2	JH0529	tumor necrosis factor	2.94e-15
17	189	14.4	234	1	OWHNS	tumor necrosis factor	2.94e-15
18	187	14.2	235	1	QJ1344	tumor necrosis factor	6.57e-15
19	187	14.2	235	2	I54490	tumor necrosis factor	6.57e-15
20	181	13.8	234	2	A25451	tumor necrosis factor	7.17e-14
21	176	13.4	235	2	JH0029	tumor necrosis factor	5.17e-13
22	175	13.3	185	2	S52715	tumor necrosis factor	7.66e-13
23	173	13.3	233	2	S24642	tumor necrosis factor	7.66e-13

24	169	12.9	233	2	S11688	tumor necrosis factor	7.97e-12
25	138	10.5	244	2	A46066	lymphotoxin beta - hu	9.00e-07
26	112	8.5	307	2	S30432	hypothetical protein	6.94e-03
27	101	7.7	384	2	S03815	probable integrase -	2.25e-01
28	100	7.6	261	2	I53476	CD40 ligand - human	3.05e-01
29	100	7.6	455	2	D69785	beta-glucosidase homo	3.05e-01
30	98	7.5	532	2	A64796	signal-transducing hl	5.57e-01
31	97	7.4	261	2	S53090	CD40 ligand - bovine	7.52e-01
32	96	7.3	528	2	T00951	hypothetical protein	1.04e+00
33	96	7.3	1022	2	I53078	homoeotic gene regulat	1.04e+00
34	95	7.3	1647	2	S45252	SNFbeta protein - hu	1.04e+00
35	95	7.2	229	2	E70405	ABC transporter - Aqu	1.36e+00
36	95	7.2	260	2	S21738	spore germination pro	1.82e+00
37	94	7.2	358	2	F69809	hypothetical protein	2.43e+00
38	93	7.1	3972	2	S75251	transforming protein	3.24e+00
39	92	7.0	527	2	A38631	Na+/H+-exchanging pro	3.24e+00
40	92	7.0	822	2	S30198	hypothetical protein	4.31e+00
41	91	6.9	245	2	S48272	sulfate adenylyltrans	4.31e+00
42	91	6.9	511	2	S55198	cytochrome-c oxidase	4.31e+00
43	91	6.9	551	2	A55582	probable iocd2 protein	4.31e+00
44	91	6.9	745	2	C70848	cation efflux system	4.31e+00
45	91	6.9	1082	2	H70360		

ALIGNMENTS

RESULT 1
 ENTRY JN0869 #type complete
 TITLE tumor necrosis factor beta - rat
 ORGANISM Rattus norvegicus #common_name Norway rat
 DATE 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Sep-1997

ACCESSIONS JN0869
 REFERENCE JN0868
 #authors Kwon, J.; Chung, I.Y.; Benveniste, E.N.
 #journal Gene (1993) 132:227-236
 #title Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
 #cross-references M01D:94040766
 #accession JN0869

##molecule_type DNA
 ##residues 1-202 ##label KWO
 ##cross-references GB:L00981; NID:q205253; PID:q205255
 ##note the authors translated codon CTC for residue 172 as ile
 COMMENT This protein is structurally related pleiotropic cytokine with
 overlapping biological functions, including an involvement in
 inflammatory processes.

GENETICS

#gene TNF-beta
 #introns 32/3; 66/1
 CLASSIFICATION #superfamily tumor necrosis factor
 KEYWORDS tumor
 SUMMARY #length 202 #molecular-weight 22111 #checksum 30955

Query Match 18.4%; Score 242; DB 2; Length 202;
 Best Local Similarity 36.5%; Pred. No. 8.30e-25;
 Matches 50; Conservative 22; Mismatches 57; Indels 8; Gaps 8;

Db	73	SLMRANTDRAFLRHFSLNNNSLIPISGLFVYSQVFSG-ES-CSP-R-A-IPT-PI	126
Qy	39	ALMHEHELGLAFTKRMNTYTNFLIPESGDFFIYSQVFRAMTSECSIRI0AGRPRKPD	98
Db	127	YLAHEVQLFSSQYFPFVPLISAKRSYPPLOGPWRSMQGVFLSKDOLSTPTDGS	186
Qy	99	SIIVVITKVTDSIPETQLMGTKSYC-EVGSNMFPQPIYLGAMFSLQESDKLNVVSDIS	157
Db	187	HLHFS-PSTVFGAFAL 202	
Qy	158	LVDTYTKEDKTFGAFALL 174	
RESULT	2	B27303	#type complete
ENTRY			

TITLE tumor necrosis factor beta precursor - mouse
 ALTERNATE_NAMES lymphotoxin; TNF beta
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 08-Sep-1997

ACCESSIONS B27303; S01342; S10083; I56004; I48853; I55980
 REFERENCE A93679
 #authors Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
 #journal Nucleic Acids Res. (1987) 15:9083-9084
 #title Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor necrosis factor) and TNF-beta-(lymphotoxin) genes.

#cross-references M01D:88067722
 #accession B27303
 #molecule_type DNA
 #residues 1-202 ##label SEM

REFERENCE S01342
 #authors Nedospasov, S.A.; Hilt, B.; Shakhov, A.N.; Dobryln, V.N.; Kawashima, E.; Accolla, R.S.; Jongeneel, C.V.
 #journal Nucleic Acids Res. (1986) 14:7713-7725
 #title The genes for tumor necrosis factor (TNF-alpha) and lymphotoxin (TNF-beta) are tandemly arranged on chromosome 17 of the mouse.

#cross-references M01D:87040736
 #accession S01342
 #molecule_type DNA
 #residues 1-11;139-160,'CG',163-178 ##label NED

REFERENCE S10083
 #authors Well, D.; Dautry, F.
 #journal Oncogene Res. (1988) 3:409-414
 #title Induction of tumor necrosis factor-alpha and -beta and interferon-gamma mRNA by interleukin 2 in murine lymphocytic cell lines.

#cross-references M01D:89144562
 #accession S10083
 #molecule_type mRNA
 #residues 6-202 ##label WEI

REFERENCE I56004
 #authors Gardner, S.M.; Mock, B.A.; Hilgers, J.; Huppi, K.E.; Roeder, W.D.
 #journal J. Immunol. (1987) 139:476-483
 #title Mouse lymphotoxin and tumor necrosis factor: Structural analysis of the cloned genes, physical linkage, and chromosomal position.

#cross-references M01D:87252204
 #accession I56004
 #status preliminary; translated from GB/EMBL/DBJ

REFERENCE I48853
 #authors Gray, P.W.; Chen, E.; Li, C.B.; Tang, W.T.; Ruddle, N.
 #journal Nucleic Acids Res. (1987) 15:3937
 #title The murine tumor necrosis factor-beta (lymphotoxin) gene sequence.

#cross-references M01D:87231097
 #accession I48853
 #status preliminary; translated from GB/EMBL/DBJ

REFERENCE I55980
 #molecule_type DNA
 #residues 1-202 ##label RE2
 #cross-references EMBL:Y00137; NID:g54842; PID:g54843

REFERENCE I55980
 #authors Li, C.
 #journal J. Immunol. (1987) 138:4496-4501
 #title Cloning and expression of murine lymphotoxin cDNA.

#cross-references M01D:87224127
 #accession I55980
 #status preliminary; translated from GB/EMBL/DBJ

#molecule_type mRNA
 #residues 1-202 ##label RE3

##cross-references GB:M16819; NID:g202088; PID:g202089
 COMMENT The first intron occurs in the 5'-untranslated region.
 GENETICS
 #gene Tnf
 #map_position 17
 #introns 32/3; 66/1
 CLASSIFICATION #superfamily tumor necrosis factor
 KEYWORDS cytokine; cytolysin; glycoprotein; lymphokine; macrophage
 SUMMARY #length 202 #molecular-weight 21998 #checksum 2011

Query Match 18.3%; Score 241; DB 2; length 202;
 Best local similarity 36.5%; Pred. No. 1.27e-24;
 Matches 50; Conservative 22; Mismatches 57; Indels 8; Gaps 8;

Db 73 SLWRASTDRAPLRHGFSNNLSLIPSGLYPVYQVFSG-ES-CSP-R-A-IPT-PI 126
 QY 39 ALHWEHELGLAFTKRNNTNKKLLIPESGDITTYISQVFRGTSCESTRAGRPNKD 98

Db 127 YLAHEVQLFESSQYPFHYPLLSAQKSYVPGIQGPRVSMYOGAVFLLSKDQSLHTDGIS 186
 QY 99 SITVITIKVTDYDEPTQLMGTKSYC-EVGSWMFQPIYLGAMFSLQEGDKLMVNSDIS 157

Db 187 HLHFS-PSSVFFCAFL 202
 QY 158 LVDTKEDKTEFFGAFLL 174

RESULT 3
 ENTRY A53062 #type complete
 TITLE Fas ligand - mouse
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Sep-1997

ACCESSIONS A53062
 REFERENCE A53062
 #authors Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nagata, S.
 #journal Cell (1994) 76:969-976
 #title Generalized lymphoproliferative disease in mice, caused by a point mutation in the Fas ligand.

#cross-references M01D:94185175
 #accession A53062
 #status preliminary

##molecule_type mRNA
 ##residues 1-279 ##label TAK
 ##cross-references GB:U06948; NID:g473564; PID:g473565

SUMMARY #length 279 #molecular-weight 31442 #checksum 3291

Query Match 17.7%; Score 232; DB 2; length 279;
 Best local similarity 35.3%; Pred. No. 5.78e-23;
 Matches 54; Conservative 32; Mismatches 50; Indels 17; Gaps 13;

Db 143 SVALHTGNPMSRS-IP-LEWEDTYGTALISG-VKRRKGGLYINENGLYFYSKVYRGO- 198
 QY 23 PVVAGTPTGHRKQFPLHWEHELGLAFTKRNNTNKKLLIPESGDITTYISQVFRGRT 82

Db 199 S-CNN--Q--P-LNH-KYVM-R-NSKYPEDVLVDEKRLNCTGTQIWAHSSYLGAVF 247
 QY 83 SECEIRQAGRPKNPDSITVITIKVDSYEPQQLMGTK-SVCEGSMWFQPIYLGAMF 141

Db 248 NLTSADHLVYNISQLSINF-EESKTFEGLYKL 279
 QY 142 SLQEGDKLMVNSDISLVDTKEDKTEFFGAFLL 174

RESULT 4
 ENTRY JH0309 #type complete
 TITLE tumor necrosis factor beta precursor - rabbit
 ALTERNATE_NAMES lymphotoxin; TNF beta
 ORGANISM #formal_name Oryctolagus cuniculus #common_name domestic rabbit
 DATE 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 29-Jan-1999

```

ACCESSIONS      JH0309; PN0098
REFERENCE        JH0309
#authors         Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.;
#journal         Nedospasov, S.A.
#file            Gene (1990) 95:215-221
#title           Structural analysis of the rabbit TNF locus, containing the
#                genes encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor
#                necrosis factor).
#cross-references M01D:91065534
#accession       JH0309
#molecule_type DNA
#residues        1-197 ##label SH2
#cross-references GB:M60341; GB:X35326; NID:g165754; PID:g165755;
#                GB:M60341; GB:X35327; NID:g165757; PID:g165758
REFERENCE        PN0098
#authors         Shakhov, A.N.; Kuprash, D.V.; Turetskaya, R.L.; Azizov, M.M.;
#journal         Andreyeva, A.V.; Nedospasov, S.A.
#file            Mol. Biol. (Mosk.) (1989) 23:1743-1750
#title           Cloning and structural analysis of the genes, coding for
#                rabbit tumor necrosis factors.
#cross-references M01D:90220566
#accession       PN0098
#molecule_type mRNA
#residues        1-197 ##label SHA
#cross-references GB:X55745; NID:g297167; PID:g297168
GENETICS
#introns         25/3; 61/1
CLASSIFICATION   #superfamily tumor necrosis factor
KEYWORDS         cytochrome; cytochrome; lymphokine; macrophage
FEATURE
1-26             #domain signal sequence #status predicted #label SIG\
27-197           #product lymphotoxin #status predicted #label MAT
SUMMARY          #length 197 #molecular-weight 21126 #checksum 8190
Query Match      17.4%; Score 229; DB 2; Length 197;
Best Local Similarity 33.6%; Pred. No. 2,05e-22;
Matches          46; Conservative 27; Mismatches 56; Indels 8; Gaps 8;
Db               68 SLRMRANTRAFLRHGFSLSNLSLLVSSGLYFYVQVFFSG-EG-CSP-K-AV-PT-PL 121
OY              39 ALHWEHELGLAFKTRNMYTKRFLIPESGDYFYQSVTRRGKMTSCSEIRQGRNKKD 98
Db               122 YLAHEVOLFSQYSFHVPILSAQSSVCPGQGPWNSVYGCANVLLTGGDQJSTHTDGA 181
OY              99 SITVITKVTDSYEPQLMTGKTSVCEVG-SNMFQPIYLGAMFSLQEGDKLKVNSYDIS 157
Db               182 HL-LTSPSSVEFGAFAL 197
OY              158 LVDYTKKEDKTFFGAFL 174
RESULT          5
ENTRY           S24641 #type complete
TITLE           lymphotoxin - bovine
ORGANISM        #format_name Bos primigenius taurus #common_name cattle
DATE            20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
                08-Nov-1996
ACCESSIONS      I46046; S24641
REFERENCE        I46046
#authors         Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans,
#journal         L.
#file            Cytokine (1993) 5:336-341
#title           Cloning and characterization of the tandemly arranged bovine
#                lymphotoxin and tumour necrosis factor-alpha genes.
#cross-references M01D:94083525
#accession       I46046
#status          preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues        1-204 ##label CL2
#cross-references EMBL:Z14137; NID:g796; PID:g797
GENETICS
#introns         32/3; 68/1
CLASSIFICATION   #superfamily tumor necrosis factor

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SUMMARY	length	204	molecular-weight	22098	checksum	9140
Query Match	17.4%	Score 229;	DB 2;	Length 204;		
Best Local Similarity	35.0%	Pred. No. 2.05e-22;				
Matches	48;	Conservative	23;	Mismatches	58;	Indels 8; Gaps 8;
DB	75	SLRRANTRDAFLRHGSLNSNLVLTPTSLTFYFSQVYSSGR-G-CFP-R-AT-PT-PL	128			
OY	39	ALHWEHELGLAFTRRMNMYTKFLIPESGDYFYFSQVTRGMTSECSERQAGRNNKD	98			
DB	129	YLAHEVOLFSQYFPHVPLLSAOKSPCPGQPVWRVSGYGAFFLLTRGDSLSTHFDGIS	188			
OY	99	SITVITVTDSYDEPQOLLMGTRVCEVG-SNNFQPIYIGAFSLQEBDKLMVYNSDIS	157			
DB	189	HL-LISPSVFEFGAFAL	204			
OY	158	LDYTKEDKTEFGAFLL	174			
RESULT	6					
ENTRY	138707	#type complete				
TITLE	Fas ligand - human					
ORGANISM	#formal_name Homo sapiens #common_name man					
DATE	29-May-1998	#sequence_revision 29-May-1998	#text_change 07-Aug-1998			
ACCESSIONS	138707; JC2340; S57565; 138554					
REFERENCE						
#authors	Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.					
#journal	Int. Immunol. (1994) 6:1567-1574					
#title	Human Fas ligand: gene structure, chromosomal location and species specificity.					
#cross-references	MUID:95127560					
#accession	138707					
#molecule_type	mRNA					
#status	preliminary: translated from GB/EMBL/DBJ					
#residues	1-281 ##label RES					
#cross-references	EMBL:011821; NID:9595430; PID:9595431					
REFERENCE						
#accession	JC2340					
#authors	Mita, E.; Hayashi, N.; Ito, S.; Takehara, T.; Hijioaka, T.; Katsuhara, A.; Fusamoto, H.; Tanaka, T.					
#journal	Biochem. Biophys. Res. Commun. (1994) 204:468-474					
#title	Role of Fas ligand in apoptosis induced by hepatitis C virus infection.					
#cross-references	MUID:95071350					
#accession	JC2340					
#molecule_type	DNA					
#residues	1-281 ##label MIT					
#cross-references	GB:D38122; DBJ:DJ9820; NID:9601892; PID:d1007898; PID:g1369902					
REFERENCE						
#accession	S57565					
#authors	Schatzlein, C.E.					
#submission	submitted to the EMBL Data Library, June 1995					
#accession	S57565					
#status	preliminary					
#molecule_type	mRNA					
#residues	1-281 ##label SCH					
#cross-references	EMBL:X89102; NID:9887455; PID:9887456					
REFERENCE						
#accession	I38554					
#authors	Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; Goodwin, R.G.; Smith, C.A.; Ramsdell, F.; Lynch, D.H.					
#journal	J. Exp. Med. (1995) 181:71-77					
#title	Fas ligand mediates activation-induced cell death in human T lymphocytes					
#cross-references	MUID:95105731					
#accession	I38554					
#status	preliminary: translated from GB/EMBL/DBJ					
#molecule_type	mRNA					
#residues	1-281 ##label RE2					
#cross-references	EMBL:U08137; NID:9624627; PID:9624628					
GENETICS						
#gene	FasL					


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#cross-references MUID::91139175
#accession 154482
#status translation not shown; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 1-124,'P',126-205 ##label RES
##cross-references GB:M55913; NID:g339742; PID:g339743
##experimental_source ancestral haplotype 57.1
#note 59-Asn was also found (ancestral haplotype 8.1)
REFERENCE
#authors Ag3350
#journal Gray, P.W.; Aggarwal, B.B.; Benton, C.V.; Bringman, T.S.;
#title Hensel, W.J.; Jarrett, J.A.; Leung, D.W.; Moffat, B.; Ng,
Nature (1984) 312:721-724
#cross-references MUID:85086243
#accession A93350
##molecule_type mRNA
##residues 1-205 ##label GRA
##cross-references GB:X01393; NID:g34444; PID:g34445
#experimental_source lymphoblastoid cell line RPM1-1788
REFERENCE
#authors A32877
#journal Goeddel, D.V.; Aggarwal, B.B.; Gray, P.W.; Leung, D.W.;
#title Nedwin, G.E.; Palladino, M.A.; Patton, J.S.; Pennica, D.;
Shepard, H.M.; Sugarman, B.J.; Wong, G.H.W.;
Cold Spring Harb. Symp. Quant. Biol. (1986) 51:597-609
#cross-references MUID:87217059
#accession B32877
##status preliminary; not compared with conceptual translation
##molecule_type mRNA
##residues 35-205 ##label GOE
REFERENCE
#authors A91906
#journal Kobayashi, Y.; Miyamoto, D.; Asada, M.; Obinata, M.; Osawa,
T.; Biochem. (1986) 100:727-733
#title Cloning and expression of human lymphotoxin mRNA derived from
a human T cell hybridoma.
#cross-references MUID:87057135
#accession A91906
##molecule_type mRNA
##residues 1-59,'N',61-205 ##label KOB
##cross-references GB:D00102; NID:g21913; PID:d100508; PID:g21914
#note the authors translated the codon TAT for residue 156 as
Thr and ACC for residue 176 as Tyr
REFERENCE
#authors A61478
#journal Fukuda, S.; Ando, S.; Sanou, O.; Tanial, M.; Fujii, M.;
#title Masaki, N.; Nakamura, K.I.; Ando, O.; Torigoe, K.;
Sugimoto, T.; Kunitomo, M.
Lymphokine Res. (1988) 7:175-185
#title Simultaneous production of natural human tumor necrosis
factor-alpha, -beta and interferon-alpha from BALL-1 cells
stimulated by HVT.
#accession A61478
##molecule_type protein
##residues 56-79,'86-95','X',97,'X',99,'119-151','XX',154-162,'X',164,
'X',166,'X',168,'X',170,'X',172-173 ##label FUK
REFERENCE
#accession S26951
#authors Voigt, C.G.; Maurer-Fogy, I.; Adolf, G.R.
#journal FEBS Lett. (1992) 314:85-88
#title Natural human tumor necrosis factor beta (lymphotoxin).
Variable O-glycosylation at Thr(7), proteolytic processing,
and allelic variation.
#cross-references MUID:93083656
#accession S26951
##molecule_type protein
##residues 35-59,'N',61-205 ##label VOI
#note 60-Thr was also found
REFERENCE
#authors S34742
#journal Fukushima, K.; Matanabe, H.; Takeo, K.; Nomura, M.; Asahi,
T.; Yamashita, K.; Arch. Biochem. Biophys. (1993) 304:144-153

```

#title	N-linked sugar chain structure of recombinant human lymphotoxin produced by CHO cells: the functional role of carbohydrate as to its lectin-like character and clearance velocity.
#cross-references MUID:	93311995
#contents	annotation
COMMENT	Secreted from mitogen-activated lymphocytes within 1-2 days after induction, this lymphotoxin can cause cytolytic effects on certain tumor cell lines and have an antiproliferative effect on others while having no detrimental effect on normal cells. It can also act synergistically with interferon gamma to kill certain transformed cell lines.
COMMENT	This protein and TNF-alpha (tumor necrosis factor) are the products of different genes closely linked on chromosome 6. They are induced by similar mitogenic stimuli and have similar biological activities but are produced by different cell types and have different induction kinetics.
GENETICS	GDB:UTA; LT; TNPB #gene #cross-references GDB:I20442; OMIM:153440 #map_position 6p21.3-6p21.3 #introns 33/3; 69/71 #note The first intron occurs before the initiator codon
CLASSIFICATION	#superfamily_tumor_necrosis_factor_cytokine; cytokine; cytotoxin; glycoprotein; homotrimer; lymphokine; macrophage
FEATURES	domain signal sequence #status predicted #label SIG product lymphotoxin #status predicted #label MAT binding_site carbohydrate (Thr) (covalent) (partial) #status experimental binding_site carbohydrate (Asn) (covalent) #status experimental
SUMMARY	#length 205 #molecular_weight 22297 #checksum 9579
Query Match	15.2%; Score 200; DB 1; Length 205;
Best Local Similarity	31.4%; Pred. No. 3,43e-17;
Matches	43; Conservative 28; Mismatches 58; Indels 8; Gaps 7;
Db	SLRANTDAPLQDDGSGSNLSLVPTSGIFVYSSOVFSCKA--YGSP-K-AT-SS-PL_129 :: :: : :: : :: :: : : : Oy 39 ALHHEHLGLAFIRKNRNNTKRLILPEBGDFIYSQTFRMTSECEINQAAGPKNPD 98
Db	YLAEHVLFSSSQPFPHVLISOSKKMYPGLOPWLMSMTHGAFOITGGDLSTHTDGIP 189 :: Oy 99 SITVVIRKVTDSDPEPTQLMGTRKYSC-EVGSNMFOPRYLGAMFLQGDKLMWVSIDS 157
Db	HLYVS-PSTVFPGAFAAL 205 : :
Oy	LVDYTKEDKTFFGAFL 174
RESULT 10	
ENTRY	S06192 #type fragment
TITLE	tumor necrosis factor alpha precursor - goat (fragment)
ALTERNATE_NAMES	cachectin; TNF alpha
ORGANISM	fomal_name Capra aegagrus hircus #common_name domestic goath
DATE	28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 08-Sep-1997
ACCESIONS	S06192; S41867
REFERENCE	S06192 Goldstein, I.M.; Henner, D.; Talhouk, A. submitted to the EMBL Data Library, March 1989
#authors	
#accession	S06192
molecule_type mRNA	
residues	1-193 ##label GOT
#cross-references EMBL:X14828; NID:g992; PID:g993	
REFERENCE	S41867 Rimstad, E. submitted to the EMBL Data Library, January 1994
#submission	
#accession	S41867
#status	Preliminary
molecule_type mRNA	


```

#residues 1-233 ##label PEN
#note this protein was isolated from the monocyte-like cell
line HL-60 from a promyelocytic leukemia

REFERENCE
#authors Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.;
Stricklier, J.; Van Arsdel, J.N.; Yamamoto, R.; Mark, D.F.
#journal Science (1985) 228:149-154
#title Molecular cloning of the complementary DNA for human tumor
necrosis factor.
#cross-references M01D:85142190
#accession A44189
#molecule_type mRNA
#residues 1-62,'S',64-233 ##label WAN
#cross-references GB:M10988; NID:g339737; PID:g339738
REFERENCE
#authors Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.;
Masaki, N.; Nakamura, K.I.; Ando, O.; Torigoe, K.;
Sugimoto, T.; Kurimoto, M.
#journal Lymphokine Res. (1988) 7:175-185
#title Simultaneous production of natural human tumor necrosis
factor alpha, -beta and interferon-alpha from BALL-1 cells
stimulated by HVJ.
#accession B61478
#molecule_type protein
#residues 83-102;109-119;121-128,'X',130-131;142-144,'X',146,
'XXX',150-152;159-174;180,'X',182-204 ##label FUK
REFERENCE
#authors Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer,
S.A.; Henzel, W.J.; Brinaman, T.S.; Nedwin, G.E.; Goeddel,
D.V.; Harkins, R.N.
#journal J. Biol. Chem. (1985) 260:2345-2354
#title Human tumor necrosis factor. Production, purification, and
characterization.
#cross-references M01D:85130974
#contents annotation: disulfide bond
REFERENCE
#authors Marmonet, A.; Fransen, L.; Tavernier, J.; Van Der Heyden,
J.; Tizard, R.; Kawashima, E.; Shaw, A.; Johnson, M.
#journal Eur. J. Biochem. (1985) 152:515-522
#title Molecular cloning and expression of human tumor necrosis
factor and comparison with mouse tumor necrosis factor.
#cross-references M01D:86030296
#accession I53311
#status translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-233 ##label RES
#cross-references GB:M26331; NID:g339763; PID:g339764
#experimental_source U-937 cells
REFERENCE
#authors Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
#journal Eur. J. Biochem. (1996) 235:431-437
#title O-glycosylated species of natural human tumor necrosis
factor-alpha.
#cross-references M01D:96202967
#accession S62610
#status preliminary
#molecule_type protein
#residues 77-99 ##label TAK
COMMENT
Secreted from mitogen-activated macrophages within 4-24 hours after
induction, TNF-alpha can cause cytotoxicity of certain tumor cell
lines and have an antiproliferative effect on others without
detriment to normal cells. It can also act synergistically with
interferon gamma to kill certain transformed cell lines.
TNF-alpha and -beta (lymphotoxin) are the products of different
genes closely linked on chromosome 6. They are induced by similar
mitogenic stimuli and have similar biological activities but are
produced by different cell types and have different induction
kinetics.
GENETICS
#gene GDB:TNF; TNFA
#map_position 6p21.3-6p21.3
#introns 62/3; 78/1; 94/1

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CLASSIFICATION	#superfamily tumor necrosis factor
KEYWORDS	cytokine; cytotoxin; glycoprotein; lymphokine; macrophage; membrane protein
FEATURE	
77-233	#product tumor necrosis factor #status experimental
145-177	#label MARY
SUMMARY	#disulfide bonds #status experimental
	#length 233 #molecular-weight 25044 #checksum 6500
Query Match	14.8%; Score 194; DB 1; Length 233;
Best Local Similarity	27.9%; Pred. No. 3,93e-15;
Matches 38; Conservative 34; Mismatches 59; Indels 5; Gaps 5	
Db	102 LOWLNRRANALLANGVELRDNOIVPSEGLYLITISQVLFKQ-G-CPST-HVLLTHITSR 158
OY	40 LHWHEHGLIAFTKRNMMNTNFKLLIPESGDYFIYSQVTFRMTSECSERIQAGRPNRPDS 99
Db	159 IAVSYQTAVNLSAIKSCQRETFEGAE-AKPWEPIYLGVPQLENGDRLSAETNRPDY 217
OY	100 ITVVI-TRVVTSTPEPTOLMGITSVCVEGSMNPQPIYLGAMFSLQSDKLMVNVSDISL 158
Db	218 LDFAESGVYFGIALL 233
OY	159 VDYTRKEDKTFFGAFL 174
RESULT 13	
ENTRY	S22052 #type complete
TITLE	tumor necrosis factor - baboon
ORGANISM	#formal_name Papio sp. #common_name baboon
DATE	20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Sep-1997
ACCESSIONS	S22052
REFERENCE	S22052
#authors	Sanjanwala, M.; Edwards, A.
#submission	submitted to the EMBL data library, September 1991
#description	Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
#accession	S22052
#status	preliminary
#molecule_type	DNA
#residues	1-233 #label SAN
#cross-references	EMBL:X62141; NID:g38159; PID:g38160
GENETICS	
#introns	62/3; 78/1; 94/1
CLASSIFICATION	#superfamily tumor necrosis factor
KEYWORDS	transmembrane protein
SUMMARY	#length 233 #molecular-weight 25557 #checksum 6746
Query Match	14.5%; Score 191; DB 2; Length 233;
Best Local Similarity	27.9%; Pred. No. 1.32e-15;
Matches 38; Conservative 34; Mismatches 59; Indels 5; Gaps 5	
Db	102 LOWLNRRANALLANGVELRDNOIVPSEGLYLITISQVLFKQ-G-CPST-HVLLTHITSR 158
OY	40 LHWHEHGLIAFTKRNMMNTNFKLLIPESGDYFIYSQVTFRMTSECSERIQAGRPNRPDS 99
Db	159 IAVSYQTAVNLSAIKSCQRETFEGAE-AKPWEPIYLGVPQLENGDRLSAETNRPDY 217
OY	100 ITVVI-TRVVTSTPEPTOLMGITSVCVEGSMNPQPIYLGAMFSLQSDKLMVNVSDISL 158
Db	218 LDFAESGVYFGIALL 233
OY	159 VDYTRKEDKTFFGAFL 174
RESULT 14	
ENTRY	I49139 #type complete
TITLE	lymphotoxin-beta - mouse
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Feb-1997
ACCESSIONS	I49139; I49138; I49076

[illegible]

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated.

Sequence: 1 MRRLSKVYSFPMRLILFL.....DISLVDYTKEDKTFGAFLL 174

Searched: 170751 seqs, 21266608 residues

Database:

Statistics: Mean 31.581; Variance 131.813; scale 0.240

SUMMARIES

Accession	Protein Name	Location/Qualifiers
R99453	standard; Protein; 174 AA.	
R99453	14-SEP-1996 (first entry)	
R99453	Tumour necrosis factor-gamma.	
R99453	Tumour necrosis factor-gamma; TNF-gamma; cancer; tumour; gene therapy; wound healing.	
R99453	Homo sapiens.	
R99453	Key	Location/Qualifiers
R99453	peptide	1..25
R99453	protein	/label= Sig.peptide 26..174
R99453	WO9614328-A1.	/label= Mat.protein
R99453	17-MAY-1996.	
R99453	07-NOV-1994; U12880.	
R99453	07-NOV-1994; WO-U12880.	
R99453	21-NOV-1994; ZA-0092228.	
R99453	(HUMA-) HUMAN GENOME SCI INC.	
R99453	NI J, Rosen CA, Yu G;	
R99453	WPI; 96-321550/32.	
R99453	N-PDB: T30390.	
R99453	Tumour necrosis factor gamma and corresponding DNA and RNA - for treating cancer, facilitating wound healing and providing resistance against infection	
R99453	Claim 1; Fig 1; 69pp; English.	
R99453	Human tumour necrosis factor-gamma (R99453) is a novel member of the TNF family. It is encoded by a cDNA clone (R30390) isolated from a human umbilical vein endothelial cell cDNA library.	
R99453	Recombinant TNF-gamma can be expressed in bacterial, insect or mammalian cells transformed with a vector carrying the TNF-gamma coding sequence. It is used to inhibit tumour cell growth, to provide resistance to infection, to induce inflammatory activity, for wound healing etc., and to screen for (ant)agonists or to raise antibodies.	
R99453	Sequence 174 AA;	

ALIGNMENTS

17	231	7.6	281_27	W21713	Human Apoptosis Induc	2.35e-11
18	231	17.6	281_23	W19777	Novel cytokine Apo-2	2.33e-11
19	231	17.6	281_23	W19787	Human apoptosis Induc	2.33e-11
20	231	17.6	281_31	W56760	Human TRAIL polypept.	2.33e-11
21	231	17.6	281_37	W76829	Human TR12 protein.	2.33e-11
22	231	17.6	281_29	W44354	Human AGR-1	2.33e-11
23	228	17.4	157_23	W10877	TNFI/TT-alpha hybrid.	4.35e-11
24	229	17.4	171_8	R41864	Bovine TNF-beta mtelet	3.56e-11
25	229	17.4	205_4	R23666	Ovine TNF-beta.	3.56e-11
26	225	17.1	239_30	W40363	Moose Fas ligand-like	8.28e-11
27	220	16.7	130_14	R79096	Human Fas ligand C-te	2.37e-10
28	220	16.7	136_33	W48955	Fas ligand fragment (2.37e-10
29	220	16.7	136_33	W48937	N-terminally deleted	2.37e-10
30	220	16.7	137_14	R79100	Human Fas ligand (par	2.37e-10
31	220	16.7	138_14	R88305	N-terminally deleted	2.37e-10
32	220	16.7	138_14	R79064	Human Fas ligand (par	2.37e-10
33	220	16.7	139_14	R88304	N-terminally deleted	2.37e-10
34	220	16.7	141_14	R88303	N-terminally deleted	2.37e-10
35	220	16.7	151_26	W16657	Human Fas ligand (hfa	2.37e-10
36	220	16.7	179_14	R79099	Human Fas ligand (par	2.37e-10
37	220	16.7	265_33	W48954	Non-cleavable Fas lig	2.37e-10
38	220	16.7	268_33	W48953	Non-cleavable Fas lig	2.37e-10
39	220	16.7	281_18	R98104	Human Fas ligand der1	2.37e-10
40	220	16.7	281_26	W21143	Human Fas ligand.	2.37e-10
41	220	16.7	281_18	R88356	Human Fas ligand.	2.37e-10
42	220	16.7	281_14	R79097	Human Fas ligand.	2.37e-10
43	220	16.7	281_14	R77281	Human Fas-L protein.	2.37e-10
44	220	16.7	281_36	W75959	Human Fas ligand.	2.37e-10
45	220	16.7	287_26	W21146	CH3/Fas ligand domain	2.37e-10

PR 10-NOV-1993; JP-305975.
PR 13-DEC-1993; JP-448256.
PR 18-MAR-1994; JP-074434.
PR 08-JUL-1994; JP-180955.
PR 07-SEP-1994; JP-239363.
PR 18-OCT-1994; JP-278378.
PA (MOCH) MOCHIDA PHARM CO LTD.
PA (OSAB-) OSAKA BIOSCIENCE INST.
PI Nagata S, Nakamura N, Suda T,
DR WPI; 95-194031/25.
N-PSDB: 094156, 099499.

PT Peptide which binds to Fas antigen, and antibody reactive with it -
 PT for treatment and diagnosis of viral or autoimmune diseases
 PS Claim 12; Fig 23-24; 300pp; Japanese.
 CC A clone (094156) contg. an insert coding for the mouse Fas ligand
 CC was isolated using probes derived from a rat Fas-L clone (see
 CC 094153). The mouse sequence contains an open reading frame coding
 CC for a 279 amino acid sequence with 5 N-glycosylation sites and a
 CC proline-rich region. The deduced mouse amino acid sequence has
 CC 91.4% homology with rat Fas-L. Fas ligands are able to induce
 CC apoptosis in cells which express the Fas cell surface antigen.
 SQ Sequence 279 AA;

Query Match 17.7%; Score 232; DB 14; Length 279;
 Best Local Similarity 35.3%; Pred. No. 1.88e-11;
 Matches 54; Conservative 32; Mismatches 50; Indels 17; Gaps 13;

Db 143 svahltpmhrs-ip-lwedtygtalssg-vkykkgslvneqglyvyskvyfrg- 198
 QY 23 PVRQPTQHFQKPFALHHEHLGLAFKRNKNTNKLIPESQDYFYSQVTFRGMT 82
 Db 199 s-cnn--q--p--lhh-kvym-r-nskypedlvimeekrllyctgqiwahssylgavf 247
 QY 83 SECSEIRQAGRNKPDSTIVITKVTDSYEPPTQLMGTRK-SVCEVGSNMFPPIYLGAMF 141
 Db 248 nltsadhlvynisqslinf-eesktffglyk 279
 QY 142 SLQEGDKLMVNVSDISLDYTKEDKTFEGAFLL 174

RESULT 15

ID W76332 standard; Protein: 279 AA.

AC W76332;
 DT 11-JAN-1999 (first entry)
 DE Human TL2 (TRAIL), ligand for TR5.
 KW TL2; TRAIL; tumour necrosis related receptor; TR5; inflammation;
 KW arthritis; septicaemia; transplant rejection; autoimmune disease;
 KW inflammatory bowel disease; graft versus host disease; infection;
 KW stroke; ischaemia; acute respiratory disease syndrome; psoriasis;
 KW restenosis; brain injury; AIDS; bone disease; cancer;
 KW atherosclerosis; Alzheimer's disease; human; therapy; diagnosis;
 KW ligand.
 OS Homo sapiens.
 PN EP-867509-A2.
 PD 30-SEP-1998.
 PR 04-FEB-1998; 300827.
 PR 28-JUL-1997; US-901469.
 PR 05-FEB-1997; US-795910.
 PA (SMK) SMITHKLINE BEECHAM CORP.
 PI Lyn SDP, Tan KB, Truneh A, Young PR;
 DR WPI; 98-497862/43.
 PT New polynucleotide encoding TR5 polypeptide - used to diagnose,
 PT prevent and treat e.g. inflammation, arthritis, septicaemia,
 PT autoimmune diseases, infections, stroke, ischaemia, ARDS, psoriasis,
 PT restenosis, brain injury, AIDS and bone diseases
 PS Disclosure; Page 17-18; 22pp; English.
 CC This is the amino acid sequence of human TL2 (also known as TRAIL),
 CC which has newly been discovered to be a ligand of human tumour
 CC necrosis related receptor TR5 (see W76331). This TR5 polypeptide
 CC of the invention and TL2 can be used in screening processes for
 CC compounds which bind the receptor, or its ligand, and which
 CC activate (agonists) or inhibit (antagonists) the receptor or TL2.
 CC Treatment of a subject with the need to inhibit TR5 polypeptide,
 CC activity comprises administering an antagonist to the polypeptide,
 CC administering a nucleic acid that inhibits the expression of the
 CC nucleotide sequence encoding the polypeptide and/or administering a
 CC polypeptide that competes with the polypeptide for its ligand,
 CC substrate or receptor. The active agents can be used for the
 CC treatment of chronic and acute inflammation, arthritis,
 CC septicaemia, autoimmune diseases (e.g. inflammatory bowel disease,
 CC psoriasis), transplant rejection, graft vs host disease, infection,
 CC stroke, ischaemia, acute respiratory disease syndrome, restenosis,
 CC brain injury, AIDS, bone diseases, cancer (e.g. lymphoproliferative
 CC disorders), atherosclerosis and Alzheimer's disease.

SQ Sequence 279 AA;

Query Match 17.6%; Score 231; DB 36; Length 279;
 Best Local Similarity 34.6%; Pred. No. 2.33e-11;
 Matches 47; Conservative 33; Mismatches 44; Indels 12; Gaps 11;

Db 152 westrsgnslsn-lhlngevlhnekqfylysgtyfr-fg-e-eikentkndk-qmv 205
 QY 42 WEHEL-GIAFTKRNMYTNKFLIPESQDYFYSQVTFRGMTSECEIRQAGRNKPDSTI 100
 Db 206 qy-lykt-sypdpdllmksarnscwskdaeyglysiyggtifefekendrffvsnhehl 263
 QY 101 TVVITKVTDSYEPPTQLMGTRKSVK-EVGSNM-FQPIYLGAMFSLQEGDKLMVNVSDISL 158
 Db 264 ld-mdeasffgaflv 278
 QY 159 VDYTKEDKTFEGAFLL 174

Search completed: Tue Jan 18 13:19:30 2000
 Job time : 68 secs.

